

# STIC Search Report Biotech-Chem Library

### STIC Database Tracking Number: 115800

TO: Diana Johannsen

Location:

Art Unit: 1634 March 3, 2004

Case Serial Number: 692077

From: P. Sheppard

**Location: Remsen Building** 

Phone: (571) 272-2529

sheppard@uspto.gov

Search Notes	
	·

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#### Sheppard, Paula

From: Sent:

Johannsen, Diana

Sent: Wednesda

To: Subject:

Wednesday, February 25, 2004 11:53 AM Sheppard, Paula

RE: 09/692,077

Hi Paula:

The search results I received in this case did not include this portion of the search:

nucleotides 880-930 of SEQ ID NO: 1 nucleotides 880-930 of SEQ ID NO: 2

I really need this part of the search since the applicant's polymorphism is located in this region. Could you check to see if this portion of the search was simply not printed or not delivered?

Thanks - I appreciate your help.

Diana

----Original Message----

From:

Sheppard, Paula

Sent: To: Tuesday, February 17, 2004 2:18 PM

To: Subject: Johannsen, Diana RE: 09/692,077

Completed today.

-----Original Message-----

From: Johannsen, Diana

**Sent:** Tuesday, February 17, 2004 10:02 AM

**To:** Sheppard, Paula **Subject:** FW: 09/692,077

Hello Paula -

Could you respond to this if possible? Any info would be appreciated (just trying to determine whether I can work on this one this biweek).

Thanks a lot.

----Original Message-----

From: STIC-Biotech/ChemLib

Sent: Tuesday, February 17, 2004 10:01 AM

**To:** Johannsen, Diana **Subject:** RE: 09/692,077

Check with Paula Sheppard.

----Original Message-----

From:

Johannsen, Diana

Sent:

Tuesday, February 17, 2004 9:54 AM

To: STIC-Biotech/ChemLib

Subject:

FW: 09/692,077

If possible, could you give me an estimate re: when this search might be complete?

Thank you very much, Diana

-----Original Message-----

From:

Johannsen, Diana

Sent:

Friday, February 06, 2004 12:04 PM

To: STIC-Biotech/ChemLib

Subject:

09/692,077

Please search the following:

0/12/04/

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Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### Result No. Score Query Match 100.0 100.0 100.0 100.0 1191 5 217323 5 232202 31533 7 18627 7 189624 7 189864 7 189864 7 189864 7 230127 7 230127 7 230213 7 268151 7 268151 7 268151 8 185321 1 186607 1 186607 2 275123 2 275122 7 206933 7 215065 7 222507 7 226214 7 287497 7 293183 9944 133405 216444 1185 Length 309 1197 30837 42003 42920 49999 49999 68233 78449 B 10 10 10 10 10 5 HUMADRAZRA AX548756 AFP005900 0 AL662790 AC069060 0 ASPA27259 0CAAR2B 0CY16189 AC108794 AC108794 AC1087260 AC085903 0 CCA427260 AC115724 AC115726 AC115726 AC115726 AC128236 AC128237 AC6111391 BCCAAR2B AC110324 AC1128094 AC1128094 AC1281994 AC1281994 AC1281994 AC129508 MUSTCE MTES05820 AC126874 4 AC145716 AC145702 AX015902 AX015908 HUMA2C2 HSA325747 IJ SUMMARIES AX548756 Sequence AF005900 Homo sapi AL662790 Mouse DNA AC069060 Mus muscu AJ427259 Anomaliru Y15946 Oryctolagus Y16189 Oryctolagus Y16189 Oryctolagus AC108794 Mus muscu AC102291 Rattus no AC102653 Rattus no AC102653 Rattus no AC105946 Rattus no AC105949 Rattus no AC115740 Mus muscu AC115748 Mouse DNA AL6218836 Rattus no AC128026 Rattus no AC128026 Rattus no AC111391 Rattus no AC110324 Rattus no AC110324 Rattus no AC110325 Equus cabal AC110325 Rattus no AC110326 Rattus no AC110327 Rattus no AC128094 Rattus no AC128094 Rattus no AC128094 Rattus no AC149777 Mus muscu AC097027 Rattus no AC149702 Rattus no AC145716 Homo sapi AC145716 Homo sapi AC145716 Homo sapi AC145702 Sequence AX015908 Sequence AX015908 Sequence AX015908 Rattus no M38742 Human a AJ325747 Homo Description AX350489 Sequence AR270618 Sequence alpha

## ALIGNMENTS

AUTHORS TITLE	REFERENCE	SOURCE ORGANISM	VERSION KEYWORDS	ACCESSION	RESULT 1 HUMA2C2 LOCUS
Chang,A.C., Ho,T.F. and Chang,N.C. In vitro amplification by polymerase chain reaction of a partial gene encoding the third subtype of alpha-2 adrenergic receptor in	bukaryota; metazoa; cnordata; craniata; vertebrata; buterteostomi; Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 885)	Homo sapiens (numan)	M38742.1 GI:177867 alpha-2 adrenergic receptor.	Human alpha-2 adrenergic receptor (ADRA2C) gene, partial cds. m38742	HUMA2C2 885 bp DNA linear PRI 06-MAR-1995

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                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1030)

Kutsenko,A.S., Gizatullin,R.Z., Al-Amin,A.N., Wang,F., Kvasha,S.M., Prodowski,R.M., Matushkin,Y.G., Gyanchandani,A., Muravenko,O.V., Levitsky,V.G., Kolchanov,N.A., Protopopov,A.I., Kashuba,V.I., Kisselev,L.L., Wasserman,W., Wahlestedt,C. and Zabarovsky,E.R. NotI flanking sequences: a tool for gene discovery and verification
2 (bases 1 to 1030)
Zabarovsky, E.R.
Direct Submission
                                                           of the human genome
Nucleic Acids Res. 22131767
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                                               12136098
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AJ325747.1 GI:15870141
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                                                                                                                                                                                                                                                                                                                                                                                     Original source text: Human adult ne Draft entry and computer-readable se kindly submitted by A.C. Chang, 20-SEP-1990.
Institute of Neuroscience 155, Sect II, Li-Noon St. Taipei, Taiwan, 11221 ROC. Location/Qualifiers
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EARD GAVPVSPASACSPPLQQPGSRVLATLRGQVLLGRGVGAIGGOWWRRRAQLTREKKFT
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(cell_type="neuroblastoma"
(tissue_type="neural"
dev_stage="adult"
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Query Match

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1 (bases 1 to 2072)
Au-Young,J. and Seilhamer,J.J.
Composition for the detection of signaling
Patent: US 6500938-A 1181 31-DEC-2002;
                                                                                                                                                                                                                                                                Unclassified.
                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 1181 from patent US AR270618
                                                                                                                                                                                                                                                                                                                                                                                        AR270618.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Alpha-2 adrenergic receptor polymorphisms
Patent: WO 0179561-A 1 25-OCT-2001;
Liggett, Stephen B. (US); Small, Kersten
Location/Qualifiers
1. .1353
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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RESULT 5
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AX548756
Sequence
AX548756
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Expansion of the alpha 2-adrenergic receptor subtype, characterization of a human alpha 2-adrenergic receptor subtype, the gene for which is located on chromosome 2

Proc. Natl. Acad. Sci. U.S.A. 87 (13), 5094-5098 (1990)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2072 bp DNA linear
Human alpha-2-adrenergic receptor (alpha-2 c2) gene,
M34041
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Original source text: Human placenta DNA, clone alpha-2 C2. Draft entry and computer-readable sequence for [1] kindly submitted by J.W.Lommaney, 03-MAY-1990, for release after publication.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 2072)
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Homo sapians (human)
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                                                                                                                                                                                                                                                                               Chromosome 2.
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                   41 from
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LPNSGQGKEGVCGASPEDBAEEEEEEEEEEEEEPAAVPVSBAACSPPLQOPGGSR
VLATLRGGVLIGRGYGAIGGGWMRRBAHVTREKGFTFVLAVVIGVFULVEPEPFBYSS
LGAICPKHCKVPHGLFQFFFWIGYCNSSLNPVIYTIFNQDFRRAFRILCRPWTQTAW
                                                                                                                                                                                                                                                                                                                                                                                      /translation="mdhqdpysvqAtaaiaaaitflilftifgnalvilavltsrslr
ReQNLFLVslaaadilvatilipfslanellgywyfbrttwcgtyaldvlfctssivh
LCAISLDRYWAVSRALEXYSKRTPBRIKCTILTVWLIAVLSLPPLIYKGDQGPOPRG
RPQCKLNQEAWYILASSIGSFFAPCLIMILVYLRIYLIAKRSNRRGPRAKGGPGQGES
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name 'ADRA2RL1'"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        organism="Homo sapiens"
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Pred. No. 0.0016;
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WO02061087.
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antigenic peptides
Patent: WO 02061087-A 41 08-AUG-2002;
Patent: WO 02061087-A 11 08-AUG-2002;
                                                                                                                                                                                                                                      Sequence update by submitter
On Aug 5, 2003 this sequence version replaced gi:2245627
Location/Qualifiers
                                                                                                                                                                                                                                                                                                               Direct Submission
Submitted (05-AUG-2003) INSERM Unit 317,
                                                                                                                                                                                                                                                                                                                                                                     3 (bases 1 to 9944)
Cayla, C., Heinonen, P.,
                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted (29-MAY-1997) INSERM Unit 317,
                                                                                                                                                                                                                                                                                                                                                                                                                                            2 (bases 1 to 9944)
Cayla, C., Schaak, S.,
Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Cayla, C., Heinonen, P., Viikari, L., Schaak, S., Snapir, A., Bouloumie, A., Karvonen, M., Pesonen, U., Scheinin, M. and P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 9944)
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Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                  Cayla,C., Heinonen,P., Vilkari,L., Schaak,S., Snapir,A., Bouloumie,A., Karvonen,M., Pesonen,U., Scheinin,M. and Paris,H.
                                                                                                                                                                                                                                                                                                                                                                                                          CHU Rangueil, Toulouse 31403, France
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Alpha2C2-adrenergic receptor gene
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens (human)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Antigenic peptides, such as for (GPCRs), antibodies thereto, and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens (human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AX548756.1 GI:25813686
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   h 100.0%;
Similarity 100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /organism="Homo sapiens"
/mol_type="unassigned DNJ
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Location/Qualifiers
                                                                                                                           clone_
                                                                                                                                                                                                  organism="Homo sapiens"
                                      gene="alpha2C2AR"
                                                                       note="alpha2C2 adrenergic
                                                                                            gene="alpha2C2AR"
                                                                                                                                              chromosome="2"
                                                                                                                                                                 db_xref="taxon:9606"
               note="adrenergic receptor
                                                                                                                                                                                                                           .9944
                                                                                                                           lib="brain fetal
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bouloumie, A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   <u>.</u>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 51; DB 6;
Pred. No. 0.0016;
                                                                                                                                                                                                                                                                                                                                                                     Viikari,L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mismatches
                                                                                                                                                                                    DNA"
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                                                                                                                            genomic
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Devedjian,J.C.
                                                                     receptor gene"
                                                                                                                                                                                                                                                                                                                                                                                                                             Institut Louis Bugnard,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 3274;
                                                                                                                                library"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          and Paris,
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polyA_signal
                                                                                                                                                           Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation manutation manutation manutation manutation manutation manutation manutation manutation manutation annotation manutation in the sequence submission only a small overlap as described above.

This sequence was finished as follows unless otherwise noted: all chemistry or covered by high quality data (i.e., phred quality sequences as compressions and repeats; all regions were cycled and repeats; all regions were covered by high quality data (i.e., phred quality as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one Mills economy that least one plasmid subclone or more than one Mills subclone; and the absenbly was confirmed by restriction digest. The following in the feature table with their source databases: Em., EMBL; Sw., database can be found at
                            http://www.sanger.ac.uk/Projects/C_elegans/wormpep RP23-53E2 is from the RPC1-23 Mouse PAC Library constructed by the group of Pieter de Jong.
For further details see http://www.chori.org/bacpac/home.htm
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       6379 GÁGGÁTGAÁGCTGAÁGAGGAGGÁAGGÁAGGÁAGGÁGGÁGGÁAGGÁAGAGTGT 6429
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Submitted (26-JUL-2002) Wellcome Trust Sanger Institute, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk On Jul 29, 2002 this sequence version replaced gi:21955513.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Center: Wellcome Trust Sanger Institute Center code: SC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Web site: http://www.sanger.ac.uk
Contact: humquery@sanger.ac.uk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 133405)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Direct Submission
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mus musculus
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Mouse DNA sequence from clone RP23-53E2 on chromosome 11, complete
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 GAGGATGAAGACTGAAGAGGAGGAAGAAGAGGAGGAAGAAGAAGAGTGT 51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         51;
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Location/Qualifiers.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   8751. .8756
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VLATTRGOVLLGRGVGATGGOWWRRAAOLTREKRPTFVLAVVIGVFVLCWFPFFFFSYS
LGATCPKHCKVPHGLFOFFFWIGYCNSSLNPVIYTIFNQDFRRAFRRILCRPWTQTAW
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APQNLFLVSLAAADILVATLIIFSLAMELLCYWYFRRTWCEVYLALDVLFCTSSIR
LCAISLDRYWAVSRALEYNSKRTPRRIKCIILTVWLIAAVISLPPLIYKGDQAPQRB
RPQKLNQCAWYILASSIGSFBAPCLIMILVYLRIYLIAKRSURRGPRAKGGPGQGES
KQPRPDHGGALASAKLPALASVASAREVNGHSKSTGEKEEGETPEDTGTRALDPSWAA
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/protein_id="AAB62558.1"
/db_xref="GI:2245628"
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Pred. No. 0.0015;
Mismatches 0
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                                                                                                                                                                                                                                                                                             REFERENCE
AUTHORS
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AUTHORS
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AUTHORS
TITLE
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JOURNAL
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ORGANISM
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VERSION
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COMMENT

source

REFERENCE

ORGANISM

AUTHORS TITLE JOURNAL

RESULT 8 AL662790

Query Match

Local

DEFINITION

ACCESSION VERSION KEYWORDS

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RESULT 9
AC069060/c
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Best Local (
Direct Submitted (17-MAY-2000) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA (15 dases 1 to 216444)

RS Birren, B., Nusbaum, C., Lander, E., Abouelleil, A., Allen, N., Boustavkiy, L., Boukhgalter, B., Corum, B., Bastien, V., Bloom, T., Collymore, A., Cook, A., Cooke, P., Corum, B., DeArellano, K., Farreira, P., FitzGerald, M., Gage, D., Galagan, J., Gardyna, S., Jodes, W., Hallo, J., Major, J., Major, J., Malor, J., Malora, T., Mlenga, V., Murphy, T., Naylor, J., O'Neil, D., Oliver, J., Peterson, K., Phunkhang, P., Pierre, N.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RS Birren, B., Linton, L., Nusbaum, C., Lander, E., Abraham, H., Allen, N., Anderson, S., Baldwin, J., Barna, N., Bastien, V., Beda, F., Anderson, S., Baldwin, J., Barna, N., Bastien, V., Beda, F., Anderson, S., Baldwin, J., Barna, N., Bastien, V., Beda, F., Anderson, S., Baldwin, J., Brown, A., Burkett, G., Compopiano, A., Castle, A., Choepel, Y., Colangelo, M., Collins, S., Collymore, A., Cooke, P., DeArellano, K., Dewar, K., Diaz, J.S., Dodge, S., Domino, M., Doyle, M., Ferreira, P., FitzHugh, W., Gage, D., Grand, Pierre, N., Graham, L., FitzHugh, W., Gayette, M., Graham, L., Grand, S., Ginde, S., Goyette, M., Graham, L., Karatas, A., Ilievi, J., Ilievi, J., Hagos, B., Heaford, A., Horton, L., Kelein, J., LaRocque, K., Lanazares, R., Landers, T., Lehoczky, J., McCarthy, M., McEwan, P., McGurk, A., McKernan, K., McCarthy, M., McEwan, P., McGurk, A., McKernan, K., McPheeters, R., Murphy, T., Naylor, J., Norman, C.H., O'Connor, T., O'Donnell, P., O'Neil, D., O'Neil, D., O'Neil, D., O'Livar, T., M., Oliver, J., Peterson, K., Pierre, N., Pisani, C., Pollara, V., Raymond, C., Riley, R., Rogov, P., Rothman, D., Stange-Thomann, N., Stojanovic, N., Subramanian, A., Talamas, J., Vassiliev, H., Viel, R., Von, A., Wilson, B., Wu, X., Wyman, D., Ye, W.J., Vong, G., Zainoun, J., Zimmer, A. and Zody, M., X., Wyman, D., Ye, W.J., Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mammalia; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 216444)
Birren,B., Nusbaum,C. and Lander,E.
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46; Conservative
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/mol type="genomic DNA"
/db_xref="taxon:10090"
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/clone_lib="RPCI-23"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 unordered pieces.
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Pred. No. 0.091;
0; Mismatches 4;
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map 11,
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WORKING DRAFT
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ROD 06-AUG-2003

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PEATURES
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (18-MAR-2003) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA ON MAR 18, 2003 this sequence version replaced gi:15291107. All repeats were identified using RepeatMasker: Smit, A.F.A. & Green, P. (1996-1997) http://ftp.genome.washington.edu/RM/RepeatMasker.html
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NOTE: This is a 'working draft' sequence. It currently consists of 6 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequencing vector: M13; M77815; 25% of reads Sequencing vector: Plasmid; n/a; 75% of reads Chemistry: Dye-terminator Big Dye; 100% of reads Assembly program: Phrap; version 0.960731 Consensus quality: 215352 bases at least Q30 Consensus quality: 215747 bases at least Q30 Consensus quality: 215851 bases at least Q30 Consensus quality: 215851 bases at least Q30 Insert size: 215944; sum-of-contigs Quality coverage: 12.0 in Q20 bases; sum-of-contigs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Center project name: L9470 Center clone name: 53_E_2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Contact: sequence submissions@genome.wi.mit.edu
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                                                                                                                                                                                                                                                                                                                                                                                                 /organism="Mus musculus"
/mol_type="genomic DNA"
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clone_end:SP6
                                                                                                                                                                                                                                                                                                       /clone="RP23-53E2"
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    note="assembly_fragment"
.38991. .216444
                                                                                                             'note="assembly_fragment"
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12927: gap of 100 bp
16633: contig of 3756 bp in length
16783: gap of 100 bp
25277: contig of 8494 bp in length
25377: gap of 100 bp
40696: contig of 15319 bp in length
40796: gap of 100 bp
138890: contig of 98094 bp in length
138990: gap of 100 bp
216444: contig of 77454 bp in length
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Rodent phylogeny and a timescale for the evolution of Glires:
evidence from an extensive taxon sampling using three nuclear genes
months. Biol. Evol. 19 (7), 1053-1065 (2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Direct Submission
Submitted (04-JAN-2002) Douzery E.J.P.,
I'Evolution, Lab. Paleonto., Paleobio.,
Montpellier II, Pl. E. Bataillon, 34 095
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Douzery,E.J.P., Delsuc,F., Stanhope,M.J. and Huchon,D. Local molecular clocks in three nuclear genes: divergence times for rodents and other mammals, and incompatibility among fossil
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3 (bases 1 to 1185)
Douzery, E.J.P.
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                                                                        AKVPTLSSPLSSAGEANGHPKPPGEKEDGETPEDPGARALPSSWAALPNSGQGQKKGA
CGASAEEEAEEEEEEEEEECEPQAVPVSPASVCSQPLQQPQGSRVLATLRGQVLLGR
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LASSIGSFFAPCLIMILVYLRIYVIAKRSNRRGPRTNGRPGQGESKQFPPVPGGAPAS
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                                                                                                                                                                                                                                                                            /product="alpha 2B adrenergic receptor"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /organism="Anomalurus sp."
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/db_xref="SPTREMBL:Q8K3R6"
                                                                                                                                                                                                                                                                                                                                                                           /gene="A2AB"
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Rodentia;
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gene for alpha 2B adrenergic receptor,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               .J.P., Institut des Sciences de
obio., Phylogenie, Universite
34 095 Montpellier Cedex 5,
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DB 10;

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Direct Submission
Submitted (16-DEC-1997) O. Madsen, University of Nijmegen,
Department of Biochemistry, PO Box 9101, NL-6500 HB Nijmegen,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Madsen, O.
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Highly congruent molecular support for a diverse superordinal clade of edemic African mammals
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Mammalia, Eutheria, Lagomorpha,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           alpha adrenergic receptor; subtype 2B oryctolagus cuniculus (rabbit) oryctolagus cuniculus
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                                                                                                                Conservative
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                                                                                                                                                                                /db_xref="$WISS-PROT:077830"
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GAMSGQMWRRRAQLSREKRFTFVLAVVIGVFVLCWFPFFFSYSLSAICPQQCRVPHG
LF"
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                                                                                                                                                                                                                                                                                                                                        /product="alpha adrenergic receptor subtype 2B"
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                                                                                                                            84.78;
93.88;
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                                                                                              Score 43.2; DB 4;
Pred. No. 0.15;
0; Mismatches 3;
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Lagomorpha; Leporidae; Oryctolagus.
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9101, NL-6500 HB Nijmegen,
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                                                                                                                                                                                                                                                                       845 GÁGGAAGAAGCTGAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGACGAG
Eukaryota; Metazoa; Chordata; Craniata; Vert
Mammalia; Eutheria; Rodentia; Sciurognathi;
1 (bases 1 to 20693)
Birren, B., Nusbaum, C. and Lander, E.
Mus musculus, clone RP23-59D8
                                                                                          HTG; HTGS_PHASE2; HTGS_DRAFT; HTGS_FULLTOP.
Mus musculus (house mouse)
Bukarrane.
Bukarrane.
                                                                                                                                                AC108794
AC108794.4
                                                                                                                                                                                AC108794 206933 bp DNA Mus musculus clone RP23-59D8, WORKING I
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Direct Submission
Submitted (12-JAN-1998) O.O.M. Madsen, University of Nijmegen,
Submitted (12-JAN-1998) O.O.M. Madsen, University of Nijmegen,
Denartment of Biochemistry, PO Box 9101, NL-6500 HB Nijmegen,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       and Springer, M.S.
Highly congruent molecular support for a diverse superordinal clade
of edemic African mammals
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      alpha adrenergic receptor.
Oryctolagus cuniculus (rabbit)
Oryctolagus cuniculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2 (bases 1 to 1183)
Madsen, O.O.M.
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                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                      /codon start=2
/codon start=2
/product="alpha adrenergic receptor subtype 2B"
/product="alpha adrenergic receptor subtype 2B"
/product="ala" (CAA76115.1"
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/db_xref="GOA:077830"
/db_xref="SWISS-PROT:077830"
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RALEN/KRTPRAK/KCIILTYWLIAAAISLPFLIYKGDQGPQHGAPQCKLNQBAYI
LSSSLGSFEYPCLIMILYYLRIATAAISLPFLIYKGDQGPQHGAPQCKLNQBAYI
AKLPTLATPVASASEANQPSKPAGEKEEGETPEDEOTQALPFGMATLPNGGQGPSAS
VGANSGSENEREEEEEBEEDPQAVPVSPASVGSPFLQQPGGSRVLATLRGQVLVGRG
VGANSGXWWRRRAQLSREKRFTFVLAVVIGVFVLCWFPFFFSYSLSAICPQQCRVPHG
LF"
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/mol_type="genomic DNA"
/db_xref="taxon:9986"
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93.8%;
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Pred. No. 0.15
0; Mismatches
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thi; Muridae; Murinae; Mus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Faro, S., Ferreira, P., FitzGerald, M., Gage, D., Galagan, J., Gardyna, S., Gord, S., Graham, L., Grand-Pierre, N., Hafez, N., Hagos, B., Horton, L., Hulme, W., Iliev, I., Johnson, R., Jones, C., Kamat, A., Karatas, A., Kells, C., Landers, T., Levine, R., Liu, G., MacLean, C., Macdonald, P., Major, J., Mindblad-Toh, K., Liu, G., MacLean, J., Meneus, L., Mihova, T., Marthews, C., McCarthy, M., Meldrin, J., Meneus, L., Mihova, T., Melega, V., Murphy, T., Naylor, J., Nguyen, C., Nicol, R., Norbu, C., Norman, C.H., O'Connor, T., O'Donnell, P., O'Neil, D., Oliver, J., Norman, C.H., O'Connor, T., O'Donnell, P., O'Neil, D., Oliver, J., Peterson, K., Phunkhang, P., Pierre, N., Raymond, C., Retta, R., Rise, C., Rogov, P., Roman, J., Roy, A., Schauer, S., Schupback, R., Seaman, S., Severy, P., Smith, C., Spencer, B., Stange-Thomann, N., Stojanovic, N., Talamas, J., Tesfaye, S., Theodore, J., Topham, K., Travers, M., Vassiliev, H., Viel, R., Vo, A., Wilson, B., Wu, X., Wassiliev, H., Viel, R., Vo, A., Wilson, B., Wu, X., Walson, B., Wu, X., Walson, B., Walson, B., Wu, X., Walson, B., Walson, 
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Birren,B., Nusbaum,C., Lander,E., Ali,A., Allen,N., Anderson,S., Barna,N., Bastien,V., Bloom,T., Boguslavkiy,L., Boukhgalter,B., Camarata,J., Chazaro,B., Chozaro,B., Chozaro,C., Choz,J.S., Dodge,S., Cook,A., Cooke,P., DeArcllano,K., Dewar,K., Diaz,J.S., Dodge,S., Farreira,P., FitzGerald,M., Gage,D., Galagan,J.,
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------ Genome Center
Center: Whitehead Institute/ MIT Center for Genome Research
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                                                                                                                                   Quality coverage: 10.1 in Q20 bases; Quality coverage: 10.1 in Q20 bases;
                                                                                                                                                                                                                                                                                                                                                                                                                  Sequencing vector: Plasmid; n/a; 100% of reads Sequencing vector: Plasmid; n/a; 100% of reads Chemistry: Dye-terminator Big Dye; 100% of reads Assembly program: Phrap; version 0.960731 (Consensus quality: 204584 bases at least Q30 (Consensus quality: 205753 (Consensus quality: 2057
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Center clone name: 59_D_8
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Insert size: 206033; sum-of-contigs
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DEFINITION
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This is a 'working draft' sequence. It currently

AC103291 215065 bp DNA linear HTG 09-NOV-2002 Rattus norvegicus clone CH230-13104, WORKING DRAFT SEQUENCE, 2

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                                                                                Similarity
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1 30760: contig of 30760 bp in length
30761 30860: gap of 100 bp
30861 31511: contig of 651 bp in length
31512 31611: gap of 100 bp
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vector_side:right"
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db_xref="taxon:10090"
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                                                              84.7%; Score 43.2; DB 2;
93.8%; Pred. No. 0.11;
tive 0; Mismatches 3;
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165128: contig
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of 32353 bp in length
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of 30524 bp in length
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AUTHORS
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Submitted (09-NOV-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
                                                                                                                                                         Submitted (24.NOV-2001) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
                                                                                                                                 Rat Genome Sequencing Consortium.
                                                                                                                  Direct Submission
                                                                                                                                                                                                                                                                                       Direct Submission
                                                                                                                                                                                                                                                                                                                  Worley, K.C.
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AC103291.5 GI.24819202
HTG, HTGS, PHASE1; HTGS_DRAFT; HTGS_FULLTOP.
Rattus norvegicus (Norway rat)
Rattus norvegicus
Chordara: Craniata; Ve;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
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211345
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On Nov 9, 2002 this sequence version replaced gi:23268227.

The sequence in this assembly is a combination of BAC based reads (http://www.hgsc.bcm.tmc.edu/projects/rat/). Each contig described in the feature table below represents a scaffold in the Atlas assembly (a 'contig-scaffold'). Within each contig described individual sequence contigs are ordered and oriented, and separated by sized gaps filled with Ns to the estimated size. The sequence contigs within a contig-scaffold that cone and there may be sequence genome shotgun sequence reads. Both ends sequences and whole table.

Center: Baylor College of Medicine

Center: Baylor College of Medicine
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NOTE: Estimated insert size may differ from sequence length (see http://www.hgsc.bcm.tmc.edu/docs/Genbank\_draft\_data.) NOTE: This is a 'working draft' sequence. It currently consists of 2 contigs. The true order of the pieces is not known and their order in this sequence record is runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it be preserved. clone end:Spb. Web site: http://www.hgsc.bcm.tmc.edu/ Contact: hgsc-help@bcm.tmc.edu Center: Baylor Co /note="wgs\_end\_extension clone\_end:Sp6" /note="wgs\_end\_extension clone\_end:Sp6" /note="wgs\_end\_extension clone\_end:Sp6"\_ end\_sequence:BH316902" 203592. .205041 202478. 203219 /note="clone\_boundary site:EcoR note="wgs\_end\_extension lone\_end:Sp6" /note="clone\_boundary clone\_end:T7 /note="wgs\_end\_extension clone\_end:T7" /organism="Rattus norvegicus"
/mol\_type="genomic DNA"
/db\_xref="taxon:10116"
/clone="CH230-13104" lone\_end ocation/Qualifiers 211244: contig of 211244 bp in length 211344: gap of unknown length 215065: contig of 3721 bp in length. it is available and the accession number will Project Information College of Medicine data.html).

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RESULT 15
AC112440
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Milosavijevic, A., Miner, G., Minja, E., Montemayor, J., Moore, S., Morgan, M., Morris, K., Morris, S., Munidasa, M., Murphy, M., Nair, L., Namkervis, C., Neal, D., Newton, N., Nguyen, N., Norris, S., Parks, K., Nwaokelemeh, O., Okwuonu, G., Olarnpunsagoon, A., Pal, S., Parks, K., Pasternak, S., Paul, H., Perez, A., Perez, L., Pfannkoch, C., Pasternak, S., Paul, H., Perez, A., Perez, L., Pfannkoch, C., Poindexter, A., Popovic, D., Primus, E., Pul, L.-L., Plugzo, M., Quiroz, J., Rachlin, E., Reeves, K., Regier, M. A., Reigh, R., Reilly, B., Reilly, M., Ren, Y., Reuter, M., Richards, S., Riggs, F., Rally, B., Reilly, M., Ren, Y., Reuter, M., Richards, S., Riggs, F., Rives, C., Rodkey, T., Rojas, A., Rose, M., Rose, R., Ruiz, S.J., Sanders, W., Savery, G., Scherer, S., Scott, G., Shatsman, S., Shen, H., Shetty, J., Shvarrebeyn, A., Sisson, I., Sitter, C.D., Smajs, D., Sned, A., Sodergren, E., Song, X.-Z., Sorelle, R., Sosa, J., Steimle, M., Strong, R., Sutton, A., Svatek, A., Tabor, P., Taylor, C., Taylor, T., Thomas, N., Thomas, S., Tingey, A., Trejos, Z., Usmani, K., Valas, R., Vera, V., Villasana, D., Waltern, L., Walker, B., Wang, J., Warren, R., Weit, X., White, F., Wang, G., Willson, R., Wleczyk, R., Wooden, H., Worley, K., Willederhausern, A., Weiss, R., Smith, D.R., Holt, R.A., Smith, H.O.,
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Rattus norvegicus
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
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AL Submitted (15 NOV-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
On Nov 15, 2002 this sequence version replaced gi:22856702.
The sequence in this assembly is a combination of BAC based reads and whole genome shotgun sequencing reads assembled using Atlas (http://www.hggc.bcm.tmc.edu/projects/rat/). Each contig described in the feature table below represents a scaffold in the Atlas assembly (a 'contig-scaffold'). Within each contig-scaffold, individual sequence contigs are ordered and oriented, and separated by sized gaps filled with Ns to the estimated size. The sequence contigs within a contig-scaffold that consist entirely of whole genome shotgun sequence reads. Both end sequences and whole genome shotgun sequence reads. Both end sequences and whole genome spatials as the sequence contigs within a contig-scaffold that consist entirely of whole sequence reads. Both end sequences and whole genome shotgun sequence only contigs will be indicated in the feature
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                                                                                                             Assembly program: Phrap; version 0.990329
Consensus quality: 206932 bases at least Q40
Consensus quality: 208648 bases at least Q30
Consensus quality: 209801 bases at least Q30
Consensus quality: 209801 bases at least Q30
Estimated insert size: 210499; sum-of-contigs estimation
Quality coverage: 7x in Q20 bases; sum-of-contigs estimation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Web site: http://www.hgsc.bcm.tmc.edu/
Contact: hgsc-help@bcm.tmc.edu
Project Information
                                                                                                                                                                                                                                                                                                                                                                                                                                  Center project name: GRYP
Center clone name: CH230-144K15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Center code: BCM
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data.html).
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* NOTE: Estimated insert size may differ from sequence length
(see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.h
NOTE: This is a 'working draft' sequence. It currently
consists of 4 contigs. The true order of the pleces
is not known and their order in this sequence record is
arbitrary. Gaps between the contigs are represented as
runs of N, but the exact sizes of the gaps are unknown.
This record will be updated with the finished sequence
soon as it is available and the accession number will
be preserved.

53078 53177: gap of unknown length
5318 53198 contig of 53077 bp in length
53198 57498: gap of unknown length
57498 164997: contig of 4221 bp in length
164998 164997: contig of 107299 bp in length
164998 122507: contig of 107299 bp in length
164998 104997: contig of 57610 bp in length
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/note="mygs contig"
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feature 57499..58533
/note="mygs contig"
feature 62821..36890
/note="mygs_contig"
feature 62821..36890
/note="mygs_contig"
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Search completed: March 2, 2004, 06:08:05 Job time : 866.5 secs 9 ORIGIN Query Match

84.7%; Score 43.2; DB 2; Length 222507;

Best Local Similarity 93.8%; Pred. No. 0.11;

Matches 45; Conservative 0; Mismatches 3; Indels 0; Gaps misc\_feature 109071. .110316 /note="wgs\_contig" 0,

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Maximum Match 100%
Listing first 45 summaries
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Perfect score:
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Aai99905 Human alp
Aad4489 Human alp
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Aag14151 Human alp
Aag14151 Human alp
Aat59499 Human alp
Aca5683 Human sig
Abz42624 Human alp
Aas68926 DNA encod
Aaz23896 Murine Lo
Aaz23891 Murine Lo
Aaac3897 Murine Lo
Aada66349 Mouse Ppp
Adb72803 Mouse Ppp
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Adb78803 Mouse Ppp
Adb78803 Human nuc
Aad65832 Human nuc
Aad44388 Human alp
Abx90802 Murine ge
Aas75442 DNA encod
Abg98152 Mouse ESd
Abx90780 Murine ge
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Genotyping determining	2001-			-APR-2000; -AUG-2000; -OCT-2000;	APR-2001;	-OCT-2001.	WO200179561-A2		sapiens	Human; genot polymorphic central nerv phosphorylat GenBank Acce	Human alpha-	FEB-2002	AAI99905;	T 1 9905 AAI99905 81		~~ ***********************************
an alpha-2B, whether an	11		LIGGETT S				1-A2.	_at	٠	SS TO TO TO TO TO TO TO TO TO TO TO TO TO	1-2BAR	2 (first		standard;		77777777777777777777777777777777777777
	70.	ı. Karı	B	2000US-00551744 2000US-00636259 2000US-00692077	2001WO-US012575			Location/Qualifier 11353 1. +tag= a "alpha-2 /product= "sequence i at nucleotides 901 (AA199906)"		; alpha alleli ystem d inosito AF0095	third i	st entry)		DNA;		1178 1956 2367 2367 2663 2663 2663 2663 2663 266
2A, ndi				174 625 207	257			)6) "		lise ol p	ntr	સુ		1353		<b>7 3 7 7 7 8 8 9 9 7 7 7 8 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4</b>
2A, or 2C adrenergic receptor gene individual is at increased risk of				9. 9.	5.			s BAR" ncludes a 9 -909 absent		<pre>ing; alpha-2B; alpha-2A; alpha-2C; adrenergic r te; allelic variant; cardiovascular disease; s system disease; adenylyl cyclase; MAP kinase n; inositol phosphate; alpha-2BAR; ion AF009500; chromosome 2; ds.</pre>	2BAR third intracellular loop encoding DNA			3 BP.	ALIGNMENTS	ACD13227  AAC38547  ABT20256  ABT20256  ABT20264  ABK65237  ACD98382  ADD30227  ADB37126  ABT19660  ABT19660  ABT19660  ABC24013  AAK52886  AAK52886  AAK51902  AAK51902  AAK51902  AAK51902  AAK51902  AAK51902  AAK51902  AAK51902  AAK51003  AAK40093  AAK40093  AAK40093  AAK40093  AAK40093  AAK40093
ntor gene useful for risk of developing a								nucleotide polymorphic site in the alpha-2BAR variant		drenergic receptor; disease; MAP kinase activity;	J DNA.					Acd13227 cDNA enco Aac38547 Arabidops Abc20256 Aspergill Abc20256 Aspergill Abc20854 Aspergill Abc20854 Aspergill Abc65237 Arabidops Acd98382 A. thalia Add30227 Plant yie Add30227 Plant yie Abc117846 Aspergill Abc1960 Aspergill Abc19660 Aspergill Abc19660 Aspergill Abc19686 Human pol Aak52886 Human pol Aak52866 Human pol Aak51902 Human pol Aak51903 DNA encod Aas92073 DNA encod Aas92073 DNA encod Aas92073 DNA encod Aas120873 Probe #10 Aba65943 Human foe Aba48060 Human bra Aba48060 Human bra Aba48060 Human bra Aba48003 Human bra Aba48003 Human bra Aba48003 Human bra

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22-OCT-1999;
                           20-OCT-2000; 2000WO-FI000913
                                                                                                              Human; cardiant; gene therapy; alpha2B-adrenoceptor; alpha2B-AR; glutamic acid repeat; intracellular loop; chromosome 2; catecholamine; norepinephrine; epinephrine; therapy; vascular contraction; coronary artery; coronary heat disease; CHD; chronic angina pectoris; acute myocardial infarction; AMI; Prinzmetal's variant; ds.
                                           26-APR-2001
                                                        WO200129082-A1.
                                                                                                           Homo sapiens
                                                                                                                                                         Human alpha2B-adrenoceptor (alpha2B-AR) gene
                                                                                                                                                                            04-JUL-2001
                                                                                                                                                                                                   AAD04762 standard; DNA; 1353
                                                                                                                                                                                                                                                                                    Sequence 1353 BP; 224 A; 458 C; 405 G; 266 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     disease associated with the corresponding receptor comprises detecting
                                                                                                                                                                                                                               51;
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                                                                                                                                                                                                                                                                      Similarity
                                                                                                                                                                          (first entry)
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              99US-00422985
                                                                   /product= "Human alpha2B-adrenoceptor (alpha2B-AR)
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                                                                                                                  Homo sapiens
                                                                                                                                               Human alpha-2B-adrenoceptor gene
                                                                                                                              hypertension;
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RESULT 2 AAD04762 ID AAD0

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Query Match Best Local Matches

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                         Heinonen P,
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Alhopuro P, Kar
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Valkonen V;
        Karvonen M,
r, Lakka TA,
    Koulu M, Peso
Nyyssoenen K;
               Pesonen
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New DNA molecule encoding variant specific adrenoceptor protein with deletion of specific amino acids located in the third intracellular lof the polypeptide, for treating vascular contraction of coronary 2001-300318/31 Kauhanen J, loop

Disclosure; Page 27-29; 37pp; English.

££x&xx3333333333333333333333333

catecholamines, norepinephrine and epinephrine. An antagonist of alpha2B-adrenoceptor is useful for treating a mammal suffering from vascular contraction of coronary arteries and a disease involving vascular contraction of coronary arteries which is clinically expressed as rinrametal's variant form or acute myocardial infarction (AMI). Alpha2B-AR gene is used in gene therapy The present sequence is a gene encoding human alpha2B-adrenoceptor (alpha2B-AR) protein. Alpha2B-AR has a glutamic acid repeat element (amino acids 298-309) of 12 glutamates, in an acidic stretch of 18 am the receptor polypeptide. Alpha2B-AR gene is located on chromosome 2. Alpha2-AR mediate many of the physiological effects of the carecholaminas normanizanhrina and minochrina a amino op of

Sequence 1353 BP; 223 A; 459 C; 405 G; 266 T; 0 U; 0 Other; 100.0%; S 100.0%; P ative 0; Score 51; DB 5; Pred. No. 0.00055; "" matches 0; Length 1353;

Indels

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Gaps

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1 GAGGATGAAGCTGAAGAGGAGGAAGAAGAGGAGGAGGAAGAAGAGTGT

standard; DNA; 1353 ВP

hypertension; alpha-28-adrenoceptor; AR; antihypertensive; hypotensive; gene; ds

Location/Qualifiers /\*tag≈ a |product= "Human alpha-2B-adrenoceptor protein"

13-FEB-2002; 2002WO-FI000113

20-FEB-2001; 2001FI-00000323

(JURI-) JURILAB LTD

Salonen

Detecting a risk of hypertension and targeting treatment in a subject determining the pattern of alleles encoding a variant alpha-2-

à

P-PSDB;

AAE26634

WPI; 2002-667063/71

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RESULT 4
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Best Local
                                                    Clone NGC-alpha2beta was isolated from a human spleen genomic library screening with a fragment of the human 5-HTIA receptor gene. The gene be used to express recombinant receptor protein which can be used to produce antibodies for inhibition of receptor function
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The invention relates to a method for detecting a risk of hypertension by determining the pattern of alleles encoding a variant alpha-2B-adrenceptor (AR) protein. The methods and compositions of the invention are useful for detecting risks and targeting treatment for hypertension. The kit is also useful for selecting for clinical drug trials testing the antihypertensive effect of compounds. The present sequence is human alpha
                                                                                                                                                                                                                                            acide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            30-OCT-1989;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             30-OCT-1989;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-OCT-1991.
                                                                                                                                                                                     Claim 1; Fig 2; 15pp;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Neurotransmission; adrenaline; epinephrine; NGC-alpha2beta; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          06-JAN-1992
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        (NEUR-) NEUROGENETIC CORP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ·2B-adrenoceptor gene
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                                                                                                                                                                                                                                         encoding
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51; Conserv
                                                                                                                                                                                                                                                                                                                         AAR14149.
                                                                                                                                                                                                                                       DNA encoding coding alpha,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                standard; DNA; 2064 BP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2 beta adrenergic receptor gene
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                                                                                                                                                                                                                                                                                                                                                                                                   Hartig
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             89US-00428856
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288. .1752
/*tag= a
                                                                                                                                                                                                                                                                                                                                                                                                   PR;
                                                                                                                                                                                                                                       human adrenergic receptor - 2-beta adrenergic receptor,
                                                                                                                                                                                        English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 51; DB 6;
Pred. No. 0.00055;
Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          266 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 1353;
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                                                                                                                                                                                                                                         for
                                                                                                                                                                                                                                       detecting
screening
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                                                                                                        c library by
The gene can
                                                                                                                                                                                                                                       nucleic drugs.
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Sequence 2064 BP; 319

Α,

696 C;

659 G;

390

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0 Other

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AATS94499
ID AATS
XX 25-N
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Best Local S
Matches 51
                                                                                                     Matches
                                                                                                                                                        Query
                                                                                                                                                                                                                                                                      A genomic DNA clone (AAT59499) codes for human alpha-2B adrenergic receptor (AAW1804), a member of the rhodopsin-like signal transducer family. It was isolated from a human spleen genomic library in the lambda vector Charon 2B by screening with a 1.6 kb fragment of the human 5-hydroxytryptamine receptor gene. Plasmid pNGC-alpha-2B comprising DNA encoding the alpha-2B adrenoceptor is deposited as ATCC 68144. Vectors have been adapted to allow prodn. of alpha-2B adrenoceptor in bacterial, yeast or mammalian cells; transfected Ltk-cells, designated L-NGC-alpha-2B, are deposited as ATCC CRL 10275. Membranes of such cells can used in novel methods to identify drugs which specifically interact with, and bind to, the alpha-2B adrenergic receptor. (Updated on 25-MAR-2003 to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Disclosure; Fig 2A-E;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            expressing recombinant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Hartig
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           25-MAR-2003
06-MAY-1997
                                                                                                                                                                                                     Sequence 2064 BP; 319 A; 696 C; 659 G; 390 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Assay for alpha-2b adrenergic receptor ligands - using
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       30-OCT-1989;
30-MAY-1991;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        21-JAN-1997
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                                                                                                                             Local
1278
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                                                  Н
                                                                                                     51;
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                                                                                                                                                                                                                                                        pr field.)
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                                                                                                                             Similarity
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                                     GAGGATGAAGCTGAAGAGGAGGAAGAGAGGAGGAGGAGGAGGAAGAGTGT
standard; DNA; 2064 BP
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                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Weinshank RL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (revised)
(first en
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         adrenergic receptor genomic DNA clone.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       89US-00428856
91US-00707604
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     9208-00965040
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288. .1751
/*tag= a
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100.0%; Pr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        receptor; adrenoceptor; adrenaline;
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                                                                                                                           100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            16pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               receptor.
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                                                                                                  Score 51; DB 2; Pred. No. 0.00056; Mismatches 0;
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Pred. No. 0.00056;
Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                88.
                                                                                                                                                   Length 2064;
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                                                                                                  Indels
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                                                                                                  Gaps
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RESULT 6
ACA56583
ID ACA5

ACA56583;

ACA56583 standard; cDNA; 2072

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RESULT 7
ABZ42624
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                                                                                                                Query Match
Best Local S
Matches 51
                                                                                                                                                                                                 CC polynucleotide probes comprising a sequence selected from one of the 1490 CC sequences mentioned in the specification. The combination is useful as an acroarray for monitoring the expression of a number of conference of the polynucleotides. The microarray is useful as an CC diagnosis and treatment of cancer and immunopathology and neuropathology. The microarray is useful in diagnostics and treatment of cancer and immunopathology and neuropathology. CC forenics and pharmacogenomics. The microarray is also useful for combination is also useful for the effects of currently available therapeutic drugs. The cc combination is also useful for profiles for the effects of currently available therapeutic drugs. The cc and genomic fragments and in research and diagnostic applications. The cc array can detect changes in expression in a large number of genes coding compathies e.g. AIDS and asthma, neuropathies e.g. Alzheimers disease. The present sequence represents a polynucleotide cc and parkinson's disease. The present sequence represents a polynucleotide cc format directly from USPNO at the printed specification but was obtained in electronic cc sequence.
                                                                                                                                                  Sequence 2072 BP, 316 A; 705 C; 660 G; 391 T; 0 U; 0 Other;
                                                                                                                                                                                     seqdata.uspto.gov/sequence.html?DocID=06500938B1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 1; SEQ ID NO 1181; 65pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Combination of polynucleotide probes, useful as array elements in a microarray for monitoring the expression of a number of target
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2003-352189/33.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Au-Young J, Seilhamer JJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              30-JAN-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (INCY-) INCYTE GENOMICS
                                                        1292
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              30-JAN-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human; probe, ss; array element; Parkinson's disease; signalling pathway population; cancer; adenocarcinoma; leukaemia; immunopathy; AIDS; asthma; neuropathy; Alzheimer's disease; microarray.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human signalling
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               06-JUN-2003 (first entry)
                                                   1 GAGGATGAAGCTGAAGAGGAGGAGGAAGAGGAGGAGGAGGAAGAGTGT
                                                                                                                51;
                            ĠĀĠĠĀŢĠĀĀĠĊŢĠĀĀĠĀĠĠĀĠĠĀĀĠĀĠĠĀĠĠĀĠĠĀĠĠĀĠĠĀĀĠĀĀĠĀĠŢĠŢ 1342
                                                                                                                          Similarity
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                                                                                                    ilarity 100.0%; S
Conservative 0;
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                                                                                            Score 51; DB 7; I
Pred. No. 0.00056;
Mismatches 0;
                                                                                                                      Length 2072;
                                                                                            Indels
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The present invention describes antigenic peptides (I) comprising: (a) CC any one of 1601 sequences (see ABPB2019 to ABBB3619) of 12-24 amino CC arids. Also described: (1) an assay for the detection of a particular GC and (2) an isolated antibody having high specificity and high affinity or an isolated antibody having high specificity and high affinity or antibodies. The particular GPCR. (I) can be used as GPCR modulators and in presence or absence of corresponding GPCRs and in the production of specific GPCRs and antibodies are useful for detecting an presence or absence of corresponding GPCRs. The antigenic peptides for CC GPCRs and antibodies are useful for detecting the treating immune-related disease, growth-related diseases, or autoimmune diseases, growth-related diseases, or autoimmune disease, e.g. AIDS, Alzheimer's diseases, call costeoarthritis, osteoporosis, cancer, cardiomyopathy, chronic and acute costeoarthritis, osteoporosis, cancer, cardiomyopathy, chronic and acute costeoarthritis osteoporosis, cancer, cardiomyopathy, chronic and acute consist, depression, schizophrenia, dementia, mental retardation, memory any other discreter in ABPA1861, dementia, mental retardation, memory can of discreter in ABPA1863 encode correction of the present invention which are used in the code correction of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Disclosure; Fig 1; 523pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New isolated antigenic peptides e.g., for G protein-coupled receptors (GPCR), useful for diagnosing and designing drugs for treating conditions in which GPCRs are involved, e.g. AIDS, Alzheimer's disease, cancer or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             G protein-coupled receptor; GPCR; antigenic peptide; gene therapy; G protein-coupled receptor modulator; antibody; immune-related disease; growth-related disease; cell regeneration-related disease; AIDS; cancer; humunological-related cell proliferative disease; autoimmune disease; alteroscierosis; infection; osteoparthritis; allergy; osteoporosis; cardiomyopathy; inflammation; Crohn's disease; diabetes; graft versus host disease; parkinson's disease; multiple sclerosis; pain; psoriasis; anxiety; depression; schizophrenia; dementia; memory loss; mental retardation; epilepsy; asthma; tuberculosis; obesity; nausea; hypertension; hypotension; renal disorder; rheumatoid arthritis; trauma;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2003-046718/04.
P-PSDB; ABP81780.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Burmer GC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (LIFE-) LIFESPAN BIOSCIENCES INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        19-DEC-2000; 2000US-0257144P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        19-DEC-2001; 2001WO-US050107
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Brown JP;
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Query Match

Sequence 3274 BP; 587 A; 979 C; 967 G; 741 T; 0 U; 0 Other;

Score 51;

DB 7;

Length 3274;

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RESULT 8
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                                                                                         CC The invention relates to isolated polynucleotide (I) and polypeptide (II)
CC sequences. (I) is useful as hybridisation probes, polymerase chain
CC reaction (PCR) primers, oligomers, and for chromosome and gene mapping,
CC and in recombinant production of (II). The polynucleotides are also used
CC in diagnostics as expressed sequence tags for identifying expressed
CC genes. (I) is useful in gene therapy techniques for restore normal
CC useful for generating antibodies against it, detecting or quantitating a
CC useful for generating antibodies against it, detecting or quantitating a
CC useful for sexpressing (II). (I) and (II) are useful in medical imaging
CC supplement. (II) and its binding partners are useful in medical imaging
CC involving aberrant protein expression or biological activity. The
CC involving aberrant protein expression or biological activity. The
CC diagnostics, forensics, gene mapping, identification of mutations
CC responsible for genetic disorders or other traits to assess biodiversity
CC and to produce other types of data and products dependent on DNA and
CC coding sequences of the invention. Note: The sequence data for this
CC patent did not appear in the printed specification, but was obtained in
CC electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              δ
 Query Match 81.6%;
Best Local Similarity 91.7%;
Matches 44; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human; chromosome mapping; gene mapping; gene therapy; forensic; food supplement; medical imaging; diagnostic; genetic disorder; ss.
                                                                  Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 1; SEQ ID NO 4730; 103pp; English.
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P-PSDB; ABG04739.
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23-AUG-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       30-MAR-2001; 2001WO-US008631
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WO200175067-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DNA encoding novel human diagnostic protein #4730
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            13-FEB-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAS68926 standard; cDNA; 291
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (HYSE-) HYSEQ INC.
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                                                                    291
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2000US-00649167.
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                                                                    129
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                                                                  A; 22 C; 112 G; 28 T; 0 U;
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   <u>.</u>
Score 41.6; DB Pred. No. 0.11; 0; Mismatches
                                 DB 5;
 4.
                                                                  0 Other;
                                 Length 291;
   Indels
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RESULT 9
AAZ23 MAZ23 MAZ23 MAZ23 MAZ23 MAZ23 MAZ2
XX AAZ2
XX AAZ2
XX Muri
XX IOBO
KW Giag
KW Spon
OX Mus
XX WO99
XX WO99
XX PA (ROS
XX CAN
XX 
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Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      bones)) encoding proteins influencing bone development in mammals. The proteins of the invention reduce and/or inactivate bone extension (i.e. development), with exception of the skull and have osteopathic activity. The nucleic acid molecules, proteins and antibodies can be used in diagnostic or pharmaceutical compounds e.g. for gene therapy. The methods and nucleic acid molecules, etc. are useful for production of transgenic animals, especially a transgenic mouse for the study of diseases associated with bone development, e.g. spondyloepiphysal dysplasia and achondroplasia. This sequence encodes the murine LOBO protein described
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LOBO; long bones; bone development; bone extension; skull; osteopathic; diagnostic; pharmaceutical; gene therapy; transgenic animal; disease; spondyloepiphysal dysplasia; achondroplasia; murine; ds.
                                                                                                              AAZ23891;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 49999 BP; 13135 A; 11787 C; 10868 G; 14209 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This invention describes novel nucleic acids (I; designated LOBO (long
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Example 3; Page 161-189; 391pp; German.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Nucleic acids encoding proteins which influence bone development, useful for treating and studying bone disorders.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   07-OCT-1999
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAZ23896;
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                                                                                                                                                                   AAZ23891
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local
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                                                                                                                                                                   standard; DNA; 49999
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  98DE-01013799.
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91.7%;
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                                                                                                                                                                                                                                                                                                                                                                                                                        Score 41.6; DB Pred. No. 0.12; 0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Wirth
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2;
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Murine LOBO genomic DNA fragment

25-JAN-2000

(first entry)

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RESULT 11
ADA66349/c
ID ADA663
XX ADA663
XX ADA663
XX AOUSE
XX AOUSE
XX AOUSE
XX CARCIT
KW CARCIT
KW KCNJ9
KW CARCIT
KW KCNJ9
KW CARCIT
KW YACCIT
KW YACCIT
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OS MUS SE
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XX
PD 03-JUI
XX OJ-JUI
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Best Local S
Matches 44
                                                                                      carcinoma-associated gene; CA gene; Rorc gene; mCG15938 gene; BAT1 gene; Iggap1 gene; IQGAP1 gene; Zpf39 gene; hCG27579 gene; KCNJ9 gene; Ppp3cc gene; PPP3CC gene; mCG9110 gene; hCG27579 gene; cancer cell; lymphatic cell; breast cell; prostate cell; epithelial cell; carcinoma-associated protein; CAP; cytostatic; gene therapy; anticancer; vaccine; carcinoma; lymphoma carcinoma; lymphatic cancer; breast cancer; breast cancer;
                            03-JUL-2003
                                                  WO2003053224-A2
                                                                                                                                                                              Mouse Ppp3cc gene genomic DNA sequence.
                                                                                                                                                                                                                                   ADA66349;
                                                                                                                                                                                                             20-NOV-2003
                                                                                                                                                                                                                                                  ADA66349 standard; DNA; 68230 BP.
                                                                                                                                                                                                                                                                                                                                                                                                               This invention describes novel nucleic acids (I; designated LOBO (long bones)) encoding proteins influencing bone development in mammals. The proteins of the invention reduce and/or inactivate bone extension (i.e., the nucleic acid molecules, proteins and antibodies can be used in diagnostic or pharmaceutical compounds e.g. for gene therapy. The methods and nucleic acid molecules, etc. are useful for production of transgenic animals, especially a transgenic mouse for the study of diseases achondroplasia. This sequence encodes the murine LOBO protein described in the method of the invention
                                                                                                                                                                                                                                                                                                                                                                                          Sequence 49999 BP; 13210 A; 11814 C; 10825 G; 14150 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Example 3; Page 69-97; 391pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Nucleic acids encoding proteins which influence bone development, useful for treating and studying bone disorders.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Rosenthal A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            27-MAR-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (ROSE/) ROSENTHAL A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mus musculus.
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                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                        (first entry)
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91.7%;
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                                                                                                                                                                                                                                                                                                                                                  Score 41.6; DI
Pred. No. 0.12
0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                         DB 2;
                                                                                  mouse; murine; ds;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Wirth T;
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Best Local :
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RESULT 12
ADA03065/c
ID ADA030
XX ADA030
AC ADA030
DT 06-NOV
XX Mouse;
KW prosta
KW prosta
XX Program
OS Mus sp
XX W02003
XX W2003
XX W200
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                                     Morris DW;
                                                                                                                                                    26-DEC-2001; 2001US-00035832
                                                                                                                                                                                                               26-DEC-2002; 2002WO-US041414
                                                                                         (SAGR-) SAGRES DISCOVERY
                                                                                                                                                                                                                                                                                                     17-JUL-2003.
                                                                                                                                                                                                                                                                                                                                                                        WO2003057146-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mouse; murine; carcinoma associated; oncogene; carcinoma; prostate; lymphoma; leukaemia; cytostatic; gene therapy; o
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mouse Ppp3cc carcinoma associated gene,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      06-NOV-2003
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2003-569168/53
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91.7%;
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0; Mismatches
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Pred. No. 0.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQ ID NO:1583.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    .12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  20634 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 68230;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    48
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WPI; 2003-587068/55

recombinant nucleic acid encoding carcinoma associated protein, ul for preparing compositions for treating carcinomas.

SEQ ID

NO 1583; 245pp; English

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RESULT 13
ADB72893/c
ID ADB728
XX ADB728
XX MOUSE
XX MOSOCI
XX MOSOCI
PR 30-JA1
XX 25-DE(
XX ASSOCI
PR 23-OC(
PR 33-NO(
PR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CC The invention relates to recombinant carcinoma associated (CA) nucleic CC acid sequences from mouse and human (ADA01492-ADA03094), and to CC carcinobinant carcinoma associated proteins (CAP) encoded by them. The CC invention also encompasses expression vectors and host cells comprising a CC cA nucleic acid, a polypeptide (especially antibody) that specifically binds to the protein, and a biochip comprising CA nucleic acid or CC fragments thereof: The sequences of the invention were identified using CC oncogenic retroviruses, which insert into the genome of the host organism CC at random. Many of these do not carry transduced host oncogens or CC gathogenic trans-acting viral genes, meaning that cancer incidence is a direct consequence of the effects of proviral integration into host CC protococogenes. The CA nucleic acid sequences can be used to diagnose CC carcinoma (especially breast cancer, prostate cancer, lymphoma or CC leukaemia) or a propensity to carcinoma by determination of the sequence CC fisuses. (A nucleic acids, proteins and antibodies are also useful as therapeutic agents and in screening and evaluating drug candidates. The CC present sequence represents a specifically claimed murine CA nucleic acid sequence of the invention. Note: The complete sequence data for this cathography from WIPO at the sequence data for this cathography is the form will an electronic format directly from WIPO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
                                                                                                                                                                                                                                  02-MAR-2001;
23-OCT-2001;
08-NOV-2001;
         WPI; 2003-239337/23
                                                               Morrie
                                                                                                                                                                                                                                                                                                                                                        26-DEC-2001; 2001WO-US051291.
                                                                                                                                                                                                                                                                                                                                                                                                                 30-JAN-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WO2003008583-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   mouse; ds; cytostatic; gene therapy; vaccine; carcinoma; lymphomas;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     04-DEC-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADB72803;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADB72803 standard; DNA; 68233
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                     (SAGR-)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LOCAL
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                                                               DW.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      44;
                                                                                                                     SAGRES DISCOVERY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    neoplasm;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   68233 BP; 18767 A; 14103 C; 14729
                                                                                                                                                                         ; 2001US-00798586.
; 2001US-00004113.
; 2001US-00052482.
; 2001US-00997722.
; 2001US-00034650.
                                                            Engelhard
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       adenocarcinoma;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ₽₽
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       sarcoma;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ŏ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 .12;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    gene.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 68233;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            48
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                                                                                                               Query Match
Best Local
                                              Matches
                                                                                                                                          in the specification. A polymucleotide of the invention has cytostatic activity, and may have a use in gene therapy, or in a vaccine. The recombinant nucleic acids and polypeptides are useful for treating carcinomas, e.g. lymphomas, cancers, neoplasm, adenocarcinoma, and sarcomas. The present sequence represents a mouse gene of the invention.
                                                                                                              Sequence 68233 BP; 18767 A; 14103 C; 14729 G; 20634 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                   Claim 1;
                                                                                                                                                                                                                                                                                                                     cancers,
                                                                                                                                                                                                                                                                                                                                     New recombinant nucleic acid, useful for treating carcinomas,
                                                                                                                                                                                                                               invention relates to a novel recombinant nucleic acid comprising a leotide sequence selected from any of the 660 sequences fully defined
                                              44;
                                                            Similarity
GAGGATGAAGCTGAAGAGGAGGAGGAGGAGGAGGAGGAGGAAGAG
                                                                                                                                                                                                                                                                                   SEQ ID NO 631; 2304pp; English
                                                                                                                                                                                                                                                                                                                   neoplasm, adenocarcinoma,
                                              Conservative
                                                          81.6%;
91.7%;
                                              0,
                                          Score 41.6; DB 9;
Pred. No. 0.12;
0; Mismatches 4,
                                                                                                                                                                                                                                                                                                                      õ
                                                                                                                                                                                                                                                                                                                      sarcomas
                                              4.
                                                                            Length 68233;
                                              Indels
            48
                                              0,
                                                                                                                                                                                                                                                                                                                                        lymphomas,
                                              Gaps
                                              0
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Complementary strand of a genomic sequence encoding a mouse
                                                                            AAL38337;
                                                                                                                  AAL38337
                                      15-AUG-2002
                                                                                                                  standard; DNA; 215980
                                      (first entry)
                                                                                                                  ВÞ
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밁

88099

66041

Cerebroprotective; neuroprotective; cytostatic; Nogo receptor homologue; NgR2; NgR3; axonal growth; central nervous system; CNS; cerebral injury; spinal cord injury; stroke; demyelinating disease; multiple sclerosis; monophasic demyelination; encephalomyelitis; Marchiafava-Bignami disease; multifocal leukoencephalopathy; panencephalitis; Spongy degeneration; Alexander's disease; Canavan's disease; metachromatic leukodystrophy; Krabbe's disease; Canavan's disease; genetic mapping; gene therapy; transgenic animal; unregulated cellular growth; cancer; tumour; mouse; murine; ds.

WO200229059-A2

11-APR-2002

06-OCT-2001; 2001WO-US031488.

06-OCT-2000; 2000US-0238361P

UNIV YALE. BIOGEN INC.

Strittmatter SM, Cate RĽ, Sah DWY;

2002-416677/44

Novel Nogo receptor homolog polypeptide, NgR2 or NgR3, useful for treating central nervous system disorder, cerebral injury, spinal treating stroke, and demyelinating diseases. cord

Example .16; Page 219-275; 277pp; English

The invention relates to a Nogo receptor homologue polypeptide, NgR3, RgR3, comprising a 50 amino acid LRRCT sequence, a 284 amino acid acid NRRCT sequence, or a 420, 461 or 392 amino acid sequence, all given in the specification. The NgR3 protein or its binding antibody is useful for decreasing inhibition of axonal growth of a central nervous system () system (CNS) ö NTLRRCT

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RESULT 15
ABQ76418/c
ID ABQ764:
XX ABQ764:
XX ABQ764:
XX ABQ764:
XX ABQ764:
XX ABQ764:
XX Bax; Bi
KW Bax; Bi
KW Vasotri
KW apopton
KW neurodd
XX Saccha:
XX WO2002:
XX 22-AUG
PM W02002:
XX 22-AUG
PF 21-DEC
XX 22-DEC
PR 22-DEC
PR 22-DEC
PR 04-JAN
XX OTANC
XX JANC
XX JANC
XX API; 2
DR PPSDB
XX PPSDB
XX WPI; 2
DR PPSDB
XX PPSDB
XX New ise
PT medicari
PT infect:
PT certain
XX Claim:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local S
Matches 44
                                                                                            New isolated nucleic acid representing a synthetic BAX-gene, useful as medicament for treating, preventing and/or alleviating yeast or fungal infections or proliferative disorders, or for preventing apoptosis in
                                                                                                                                                                                                                                                                                                                      Contreras RH,
                                                                                                                                                                                                                                                                                                                                                                                                                                  22-DEC-2000; 2000EP-00870318.
04-JAN-2001; 2001EP-00870002.
09-JAN-2001; 2001EP-00870003.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bax; Bax-resistance; cytostatic; fungicide; immunosuppressive; virucide; vasotropic; vaccine; gene therapy; proliferative disorder; cancer; apoptosis; fungal; yeast; infection; autoimmune disease; ischaemia; neurodegeneration; cell death; ss.
                                                                                                                                                                                                                                                                                                                                                                           (JANC ) JANSSEN PHARM NV.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    21-DEC-2001; 2001WO-EP015398
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WO200264766-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Saccharomyces cerevisiae.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        S. cerevisiae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ABQ76418 standard; cDNA; 1721
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  21-NOV-2002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2002-667002/71.
DB; ABG93152.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (first entry)
                                                                                                                                                                                                                                                                                                                   Eberhardt I,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BAX-associated cDNA fragment SEQ ID 261.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       81.6%; Score 41.6; DB 91.7%; Pred. No. 0.13;
                                                                                                                                                                                                                                                                                                             Luyten WHML,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Mismatches
                                                                                                                                                                                                                                                                                                                Reekmans
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 215980;
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Claim 36; Fig 1; 344pp; English

В Ś

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CC This invention describes a novel nucleic acid representing a synthetic CC Reax gene. The Bax gene of the invention is useful for identifying Bax-cc candida spp. sequences that are differentially expressed in a pathway CC inhibitor sequences of Bax-induced cell death or identifying inhibitors or control activity and can be used in vaccines or for gene therapy. The CC invention have cytostatic, fungicide; immunosupressive, virucide and CC isolated nucleic acids, polypeptides, pharmaceutical compositions, CC antisense molecules and antibodies are useful as medicaments or in CC diseases associated with yeast or fungi or proliferative disorders, such CC or polypeptides, or the genetically modified organism are useful for CC as cancer, or for preventing apoptosis in certain diseases. The compounds CC preparing a medicament for modifying the endogenic flora of humans and CC preparing a medicament for modifying the endogenic flora of humans and content of the compounds of the compounds of the compounds of the content is useful for immunising against yeast or content mammals. The vaccine is useful for immunising against yeast or fings infections or neurodegenerations. The content of the invention of the save gene content of the disclosure of the invention or neurodegenerations.
1721
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В Ś Query Match Best Local S Matches 43 631 GAAGATGAAGAAGAAGAGGAGGAGGAGGAGGAGGAGGAAGA 585 43; 1 GAGGATGAAGCTGAAGAGGAGGAGGAAGAAGAGAGGAGGAGGAAGA 47 Similarity Conservative BP; 501 A; 400 C; 341 G; 479 T; 0 U; 0 Other; 79.6%; 91.5%; ; Score 40.6; DB; Pred. No. 0.2; 0; Mismatches BG 4. Length 1721; Indels 0 Gaps

0

Search completed: March Job time: 267.5 secs 2004, 05:39:00

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Result
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Sequence:
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Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Minimum DB seq length:
Maximum DB seq length:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Total number of hits satisfying chosen parameters:
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    Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                       Score
    nucleic search, using sw model
    Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      March 2, 2004, 05:39:14; Search time 60 Seconds (without alignments) 471.708 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        682709 seqs, 277475446 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             IDENTITY_NUC Gapop 10.0 , Gapext 1.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-09-692-077D-1_COPY_880_930
51
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                                                                                                                                                                                                                                                                                                                                                                                                     gaggatgaagctgaagagga.....aggaggaggaggaagagtgt
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GenCore version 5.1.6 Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                                                                                                                                                                                                                                       Length
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   636
636
636
1194
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           US-09-016-434-1181
US-09-533-029-47
US-09-533-029-168
US-09-736-457-168
US-09-713-25-168
US-09-614-124B-168
US-09-614-133-31
US-08-860-038-15
US-08-860-038-16
US-09-580-923-15
US-08-860-038-16
US-09-163-285-3
US-09-163-285-3
US-09-163-285-3
US-09-702-705-788
US-09-702-705-788
US-09-614-124B-788
US-09-614-124B-788
US-09-614-124B-788
US-09-614-124B-788
US-09-614-124B-788
US-09-614-124B-788
US-09-614-124B-788
US-09-614-124B-788
US-09-613-25-788
US-09-614-124B-788
US-09-613-125-788
US-09-613-125-788
US-09-613-125-788
US-09-620-312D-1085
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Sequence 1181, Ap
Sequence 1668, Ap
Sequence 1668, Ap
Sequence 1668, Ap
Sequence 1668, Ap
Sequence 33, App
Sequence 31, Appl
Sequence 15, Appl
Sequence 16, Appl
Sequence 16, Appl
Sequence 34, Appl
Sequence 34, Appl
Sequence 31, Appli
Sequence 316, App
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Query Match.
Best Local Similarity

100.0%;

Score 51; Pred. No.

DB 4; Length 2072;

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	TILING DATE: HEREWITH CLASSIFICATION DATA: APPLICATION APPLICATION POPULAR COMPOTER DATA: APPLICATION POPULAR OF SEQUENCES: 1490 CORRESPONDENCE ADDRESSES INVENTION POPULAR OF SEQUENCES: 1490 CORRESPONDENCE ADDRESSES INVENTION POPULAR DATA: APPLICATION POPULAR COMPOTER DATA: APPLICATION NUMBER: US/09/0 FILING DATE: HEREWITH CLASSIFICATION DATA: APPLICATION NUMBER: US/09/0 FILING DATE: HEREWITH CLASSIFICATION DATA: APPLICATION NUMBER: US/09/0 FILING DATE: HEREWITH CLASSIFICATION: THE SECUENCE SOCIETY AGENT INFORMATION: TELEPHONE: (650) 855-0555 TELEPHONE: (650) 855-0555 TELEPHONE: (650) 855-0555 TELEPHONE: (650) 855-0555 TELEPHONE: GENBANK CLONE: GENBANK CLONE	43676 511259 51259 2609 2669 2669 2659 3255 3630 3630 3630	5573
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	34 FOR THE DET EXPRESSION Windows/MS 434	356-618-781-5618-781-5618-781-561-561-561-561-561-561-561-561-561-56	418-7
1	OR THE DETECTION EXPRESSION LLS, INC. Windows/MS-DOS 6	714C-5 991-209 166-209 1212-7 1212-9 1212-9 1212-9 1212-5 1212-5 1212-1 1212-1 1212-1 1212-1 1212-1 1212-1 1212-3 1212-3 1212-3 1212-3 1212-3	10-30
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APPLICANT: Fan, Liqun
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
TITLE OF INVENTION: DIAGNOSIS OF LUNG CANCER
FILE REFERENCE: 210121.478C14
CURRENT APPLICATION NUMBER: US/09/702,705
CURRENT FILLING DATE: 2000-10-30
NUMBER OF SEQ ID NOS: 1833
SOFTWARE: FastSEQ for Windows Version 3.0
LENGTH: 636
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; OTHER INFORMATION: G1089 US-09-533-029-47
                                                                                                                                                                                                                                                                                      Sequence 1668, Application US/09702705 Patent No. 6504010
                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
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CURRENT FILING DATE: 2000-03-22
EARLIER APPLICATION NUMBER: 60/125,814
EARLIER FILING DATE: 1999-03-23
NUMBER OF SEQ ID NOS: 121
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 47
SEQ ID NO 47
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APPLICANT: Jiang, Cai-Zhong
APPLICANT: Neuber, Lynne
TITLE OF INVENTION: DISEASE-INDUCED POLYNUCLEOTIDES
FILE REFERENCE: MBI-010
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ORGANISM: Arabidopsis thaliana
REATURE:
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APPLICANT: Pineda, Omaira
                                                                                                                                                                                                                                                                  INFORMATION:
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Vedvick, Tom
Carter, Darrick
Retter, Marc
Mannion, Jane
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Lodes, Michael A.
                                                                                                                                                                                                                                 Wang, Tongtong
Bangur, Chaitanya
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89.6%;
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Pred. No. 0.019;
0; Mismatches
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US-09-614-124B-1668
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NUMBER OF SEQ ID NOS: 1668
SOFTWARE: FASTSEQ for Windows Version 3.0
SEQ ID NO 1668
LENGTH: 636
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; ORGANISM: Homo sapiens
US-09-702-705-1668
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                                                     APPLICANT: Fanger, Gary
APPLICANT: Vedvick, Tom
APPLICANT: Carter, Darrick
APPLICANT: Carter, Darrick
APPLICANT: Mannion, Jane
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THERAPY AND
TITLE OF INVENTION: DIAGNOSIS OF LUNG CANCER
FILE REFERENCE: 210121.478C9
CURRENT APPLICATION NUMBER: US/09/614,124B
CURRENT FILING DATE: 2001-07-11
                                                                                                                                                                                                                                                               Sequence 1668, Application US/09614124B Patent No. 6630574
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SOFTWARE: FastSEQ for
SEQ ID NO 1668
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APPLICANT: Bangur, Chaitanya
APPLICANT: Lodes, Michael A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TITLE OF INVENTION: COMPOSITIONS AND METHODS TITLE OF INVENTION: DIAGNOSIS OF LUNG CANCER CILE REFERENCE: 210121.478C15
CURRENT APPLICATION NUMBER: US/09/736,457
CURRENT FILING DATE: 2000-12-13
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APPLICANT:
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APPLICANT:
APPLICANT:
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LENGTH: 63
TYPE: DNA
                                                                                                                                                                                                                                                                                                                                          42;
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Similarity 87.5%;
42; Conservative
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Retter, Marc
Mannion, Jane
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Wang, Aijun
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Lodes, Michael
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Sequence 333, Application US/09328111
Patent No. 6262333
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Matches 42; Conservative
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                                                               APPLICANT: Ford, Donna M.
APPLICANT: Lewis, Marcia E.
APPLICANT: Monahan, John E.
APPLICANT: Schlegel, Robert
TITLE OF INVENTION: NOVEL HUMAN GENES AND GENE EXPRESSION
TITLE OF INVENTION: PRODUCTS
FILE REPERENCE: CCD-257 (US)
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TYPE: DNA
ORGANISM: Homo sapiens
09-671-325-1668
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                              CURRENT APPLICATION NUMBER: US/09/328,111
CURRENT FILING DATE: 1999-06-08
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APPLICANT: Steinmann, Kathleen E.
APPLICANT: Astle, Jon H.
                                                                                                                                                                                                                                   PPLICANT: Bushnell, Steven E.
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                                                                                                                                                                                                   PPLICANT: Carroll III, Eddie PPLICANT: Catino, Theodore J.
   ARLIER APPLICATION NUMBER: US 60/088,801
ARLIER FILING DATE: 1998-06-10
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42; Conser
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Retter, Marc
Mannion, Jane
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Bangur, Chaitan
Lodes, Michael J
Fanger, Gary
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1998-06-10
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87.5%;
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87.5%;
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Pred. No. 0.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mismatches
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0.045;
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                                                                                                                                                                                                                                                                                                                               RESULT 9
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; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-220-132-31
                                                                                                                                                                                                                                                                                                                 US-08-860-038-15
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                                                                                                                                                                                                                                                                             Sequence 15, Application US/08860038 Patent No. 6287762
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: FastSEQ for Windows Version 3.0 SEQ ID NO 333
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 73.3%;
Best Local Similarity 87.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQ ID NO 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CURRENT APPLICATION NUMBER: US/09/220,132
CURRENT FILING DATE: 1998-12-23
PRIOR APPLICATION NUMBER: US 60/079,303
PRIOR FILING DATE: 1998-03-25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQ ID NOS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Shyjan, Andrew W.
TITLE OF INVENTION: METHODS AND COMPOSITONS FOR TITLE OF INVENTION: OF PROSTATE CANCER THERAPIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FEATURE:
NAME/KEY: misc_feature
LOCATION: (1)...(650)
OTHER INFORMATION: n = A,T,C or G
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 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
COMPUTER: IBM PC com
                                                                                                                                                                                                              APPLICANT: CROUZ
APPLICANT: SCHER
APPLICANT: WILS,
                                                                                                                                              CORRESPONDENCE ADDRESS:
                                                                                                                                                                             TITLE OF INVENTION: PURIFICATION OF A TRIPLE HELIX FORMATION TITLE OF INVENTION: WITH AN IMMOBILIZED OLIGONUCLECTIDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LE REFERENCE:
                                                                                                               STREET:
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                                                                                                                               ADDRESSEE:
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No. 6506607
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                                                 19426
                                                                                            SSEE: Rhone-Poulenc Rorer Inc.
T: 500 Arcola Road, Mailstop 3C43
Collegeville
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FastSEQ for Windows Version 4.0
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                                                                  USA
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SCHERMAN, Daniel
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1997-12-24
compatible
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Pred. No. 0.085;
0; Mismatches 6;
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Pred. No. 0.045;
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OF PROSTATE CANCER
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US-08-860-038-16/c
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                                       FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: FR 94/
FILING DATE: 16-DEC-1994
PRIOR APPLICATION DATA:
CONTROL OF THE CONTROL OF T
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      sequence 16,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches
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Best Local (
APPLICATION NUMBER: WO FR95/01468 FILING DATE: 08-NOV-1995 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEFAX: (610) 454-3808
INFORMATION FOR SEQ ID NO: 1
SEQUENCE CHARACTERISTICS:
LENGTH: 58 base pairs
                                                                                                                                                     SOFTWARE: Patentin Release #1.0, CURRENT APPLICATION DATA:
                                                                                                                                                                                                                        COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TOPOLOGY: lir
MOLECULE TYPE:
DESCRIPTION:
                                                                                                                                                                                                                                                                                                                CORRESPONDENCE ADDRESS:
ADDRESSEE: Rhone-Poulenc Rorer Inc.
STREET: 500 Arcola Road, Mailstop 3C43
                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: CROUZET, Joel
APPLICANT: SCHERMAN, Daniel
APPLICANT: WILS, Pierre
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ent No.
                                                                                                                                                APPLICATION NUMBER:
                                                                                                                                                                                         COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                          CITY: Collegeville
                                                                                                                                                                                                                                                                                                                                                                            ITLE OF INVENTION: PURIFICATION OF A TRIPLE HELIX FORMATION ITLE OF INVENTION: WITH AN IMMOBILIZED OLIGONUCLEOTIDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME: SAVITZKY EBQ., MARTIN F. REGISTRATION NUMBER: 29,699
REFERENCE/DOCKET NUMBER: ST940:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (610) 454-3816
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: WO FIFILING DATE: 08-NOV-1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION DATA,
APPLICATION NUMBER: FR 9.
FILING DATE: 16-DEC-1994
PRIOR APPLICATION DATA,
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                                                                                                                                                                                                                                                                                                                                                                         MBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      INFORMATION:
                                                                                                                                                                                                                                                                  19426
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187762
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/desc = "Oligonucleotide"
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                                                                             FR 94/15162
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n_Release #1.0, Version
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Pred. No. 0.099;
0; Mismatches 7;
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                                                                                                                                                                      Version #1.30
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                                                                                                                                          RESULT 12
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SEQ ID NO 15
LENGTH: 58
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
                                                                                                                                                                                                                                                                                                   US-09-580-923-15
                                                                                                                                                                                                                                                                                                                                                                                                        FILE REFERENCE: 03804.0138-01
CURRENT APPLICATION NUMBER: US/09/580,923
CURRENT FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: 08/660,038
PRIOR FILING DATE: 1997-06-09
PRIOR PPLICATION NUMBER: PCT/FR95/01468
PRIOR FILING DATE: 1995-11-08
                                                           GENERAL INFORMATION: APPLICANT: Crouzet
                                                                                            Sequence 1
Patent No.
                                                                                                                                                                                                                                          Matches
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US-09-580-923-15
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APPLICANT: Scherman, Daniel
APPLICANT: Scherman, Daniel
APPLICANT: Wils, Pierre
APPLICANT: Cameron, Beatrice
APPLICANT: Blanche, Francis
TITLE OF INVENTION: PURIFICATION OF A TRIPLE HELIX FORMATION WITH AN
TITLE OF INVENTION: IMMOBILIZED OLIGONUCLEOTIDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEPHONE: (610) 454-38:
TELEPAX: (610) 454-3808
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                     Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MOLECULE TYPE:
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REFERENCE/DOCKET NUMBER: ST
TELECOMMUNICATION INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LENGTH: 58 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local
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                                                                                           16, Application US/09580923
o. 6319672
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                                                                                                                                                                     Scherman, Daniel
Wils, Pierre
              Cameron, Beatrice
                                                           Crouzet, Joel
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/desc = "Oligonucleotide"
Francis
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85.4%;
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85.4%;
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Pred. No. 0.09
0; Mismatches
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Pred. No. 0.099;
0; Mismatches 7;
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RESULT 14
US-09-163-285-3
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US-09-894-998A-34/c
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SEQ ID NO 16
LENGTH: 58
TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Sleath, Paul R.

TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE DIAGNOSIS AND TITLE OF INVENTION: TREATMENT OF HERPES SIMPLEX VIRUS INFECTION FILE REFERENCE: 210121.538

CURRENT APPLICATION NUMBER: US/09/894,998A

CURRENT FILING DATE: 2001-06-28

NUMBER OF SEQ ID NOS: 64

SOFTWARE: PastSEQ for Windows Version 4.0

SEQ ID NO 34

LENGTH: 661
                                                                                                                                                      Sequence 3, Application US/09163285 Patent No. 6204013
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 34, Application US/09894998A Patent No. 6537555
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GENERAL INFORMATION:
APPLICANT: Khodadoust, Mehran
APPLICANT: Khodadoust, Mehran
TITLE OF INVENTION: MOVEL MSP-5 PROTEIN AND NUCLEIC ACID MOLECULES
TITLE OF INVENTION: AND USES THEREOF
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESS: LAHIVE & COCKFIELD, LLP
STREET: 28 State Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Hosken,
APPLICANT: Craig I
APPLICANT: Davin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION NUMBER: PCT, PRIOR FILING DATE: 1995-11-08 NUMBER OF SEQ ID NOS: 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CURRENT APPLICATION NUMBER: US/09/580,923
CURRENT FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: 08/860,038
PRIOR FILING DATE: 1997-06-09
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: DNA
ORGANISM: HSV-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FEATURE: OTHER INFORMATION: Description of Artificial Sequence: OTHER INFORMATION: oligonucleotide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                    Local Similarity 85.4 nes 41; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Match 72.2%;
Local Similarity 85.4%;
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Davin C. Dillon
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85.4%;
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Pred. No. 0.12;
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                                                                                                                                                                                                                                                                                                                                      Mismatches
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US-09-163-285-1
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 227-7400
TELEPAX: (617) 742-4214
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 1, Application US/09163285 Patent No. 6204013
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches
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APPLICANT: Khodad
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/0:
FILING DATE: June 24, 19:
ATTORNEY/AGENT INFORMATION:
                                 CLASSIFICATION:
PRIOR APPLICATION DATA:
                                                                                SOFTWARE: PatentIn Release #1.0, Version CURRENT APPLICATION DATA: APPLICATION NUMBER: US/09/163,285
                                                                                                                                                                                  COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                   CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD, LLP
STREET: 28 State Street
                                                                                                                                                                                                                                                                                                                                       TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOPTWARE: PatentIn Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME/KEY:
LOCATION:
                                                                                                                               MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDIUM TYPE: Ploppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
APPLICATION NUMBER: 60 FILING DATE: June 24,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CITY: Boston
STATE: Massa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRANDEDNESS:
TOPOLOGY: lir
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME: Mandragouras, Amy E. REGISTRATION NUMBER: 36,20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ZIP: 02109
                                                                    FILING DATE
                                                                                                                                                                                                                   COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           628
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 GAGGATGAAGCTGAAGAGGAGGAGGAGGAGGAGGAGGAGGAAGAG 48
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                                                                                                                                                                                                                                                   Boston
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               60/090,398
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Pred. No. 0.12;
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                                                                                                                     #1.25
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0,

NAME: Mandragouras, Amy E.
REGISTRATION NUMBER: 36,207
REFERENCE/DOCKET NUMBER: MNI-049
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)227-7400
TELEPHONE: (617)227-7400
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1512 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
MOLECULE TYPE: cDNA
FRATURE:
FRATURE:
COATION: 125..868
US-09-163-285-1 Search completed: March 2, 2004, 08:36:49 Job time : 61 secs В Query Match 72.2%; Score 36.8; DB 3; Length 1512; Best Local Similarity 85.4%; Pred. No. 0.12; Matches 41; Conservative 0; Mismatches 7; Indels 0; Gaps 0,

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Result
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Maximum DB seq length: 200000000
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Maximum Match 100%
Listing first 45 summaries
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Searched:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Published Applications NA:*

1: /cgn2 6/ptodata/2/pubpna/US07 PUBCOMB.seq:*

2: /cgn2 6/ptodata/2/pubpna/PCT_NEW PUB.seq:*

3: /cgn2 6/ptodata/2/pubpna/US06 NEW PUB.seq:*

4: /cgn2_6/ptodata/2/pubpna/US06_PUBCOMB.seq:*

4: /cgn2_6/ptodata/2/pubpna/US07_NEW PUB.seq:*

7: /cn2_6/ptodata/2/pubpna/US07_NEW PUB.seq:*
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Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /cgn2_6/ptodata/2/pubpna/US09E_PUBCOMB.seq:*
/cgn2_6/ptodata/2/pubpna/US09C_PUBCOMB.seq:*
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6 68233
6 215980
8 1344
1344
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223
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14 US-10-077-870-3
14 US-10-071-073-1
15 US-10-305-720-1181
14 US-10-225-5678-41
15 US-10-234-650-31
10 US-09-972-646-16
9 US-09-972-644-146
9 US-09-728-444-146
9 US-09-728-444-124
12 US-10-161-927-81
15 US-10-161-927-83
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                                 Sequence 3, Appli
Sequence 3, Appli
Sequence 1, Appli
Sequence 11, Appli
Sequence 41, Appl
Sequence 31, Appli
Sequence 1, Appli
Sequence 1, Appli
Sequence 146, App
Sequence 146, App
Sequence 147, App
Sequence 1420, App
Sequence 124, App
Sequence 124, App
Sequence 124, App
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US-09-954-456-308 US-10-418-182-296	US-10-120-988-114	US-10-175-523-97	US-09-818-264-3	US-10-227-577-1892	US-10-091-504-1892	US-09-764-869-1892	US-10-175-523-184	-10-027-632-	US-10-027-632-103743	-10-027	-10-102-806-	US-09-893-519A-115	US-10-211-859-4	US-10-029-386-4279	US-09-864-761-1597	US-09-864-761-18355	US-10-029-386-17979	US-10-128-714-5204	US-10-128-714-204	US-10-374-780A-229	-10	US-10-225-068-65	US-09-934-455-177	US-09-533-029-47	US-10-128-714-7204	US-10-128-714-6204	-114-	US-10-424-599-47976
Sequence 308, App Sequence 296, App	Sequence 114, App	9	Sequence 3, Appli	ш	e 1892	1892,	Sequence 184, App	e 1117	Sequence 103743,	9763		115,		e 42	1597	18359	1797	5204	204,	229,	Sequence 45, Appl	65,	e 177	e 47,	e 720	Sequence 6204, Ap	194:	Sequence 47976, A

## ALIGNMENTS

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US-09-825-923-3

Sequence 3, Application US/09825923

Patent No. US2001001633BA1

GENERAL INFORMATION:

APPLICANT: Snapir, Amir

APPLICANT: Snapir, Amir

APPLICANT: Helmonen, Paula

APPLICANT: Koulu, Marku

APPLICANT: Koulu, Marku

APPLICANT: Koulu, Marku

APPLICANT: Koulu, Marku

APPLICANT: Salonen, Jukka T

APPLICANT: Salonen, Jukka T

APPLICANT: Salonen, Tomi-Pekka

APPLICANT: Salonen, Kristina

APPLICANT: Salonen, Nussi

APPLICANT: Kanhanen, Jussi

APPLICANT: Kanhanen

APPLICANT: Kan
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RESULT 4
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; NAME/KEY: CDS
; LOCATION: (1)..(1350)
; OTHER INFORMATION: Coding sequence for human alpha-2B-adrenoceptor protein
.US-10-077-870-3
                                                                                                                                                                                                                                                                                                                                                                                                                                               US-10-001-073-1
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                                                                                                       Query Match 100.
Best Local Similarity 100.
Matches 51; Conservative
                                                                                                                                                                                                                                                                                                                        Sequence 1, Application US/10001073
Publication No. US20030113725A1
GENERAL INFORMATION:
APPLICANT: Liggett, Stephen
APPLICANT: Small, Kirsten
TITLE OF INVENTION: Alpha-2-adrenergic receptor polymorphisms
FILE REFERENCE: 13073-PCT
                                                                                                                                                                                                                                            SOFTWARE: PatentIn Ver. SEQ ID NO 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 100.
51; Conservative
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CURRENT FILING DATE: 2001-11-01
NUMBER OF SEQ ID NOS: 53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 3, Application US/10077870 Publication No. US20030003470A1 GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
Matches 51; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Salonen, Jukka T
TITLE OF INVENTION: Method for detecting a risk
FILE REFERENCE: 0933-0183P
CURRENT APPLICATION NUMBER: US/10/077,870
CURRENT FILING DATE: 2002-05-21
PRIOR APPLICATION NUMBER: FI 20010323
PRIOR APPLICATION NUMBER: F0 20010323
PRIOR FILING DATE: 2001-02-20
NUMBER OF SEQ ID NOS: 10
SOFTWARE: Patentin Ver. 3.1
                                                                                                                                                                                           LENGTH: 1353
TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH: 1353
TYPE: DNA
ORGANISM: Homo sapiens
                                               980
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      880 GAGGATGAAGCTGAAGAGGAGGAAGAGGAGGAGGAGGAGGAAGAGTGT 930
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 GAGGATGAAGCTGAAGAGGAGGAAGAGGAGGAGGAGGAAGAAGAGTGT
                                    GAGGATGAAGCTGAAGAGGAGGAAGAGGAGGAGGAGGAGGAAGAGTGT 930
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                     100.0%; Score 51; DB 14; 100.0%; Pred. No. 9.7e-06; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          100.0%; Score 51; 100.0%; Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        100.0%; Score 51; DB 9; 100.0%; Pred. No. 9.7e-06;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            9.7e-06;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 of hypertension and uses thereof
                                                                                                                                       Length 1353;
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                                                                                                     Gaps
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US-10-305-720-1181

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                                                                                                                                                                                                             RESULT 6
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FEATURE:
NAME/KEY: misc_feature
OTHER INFORMATION: GenBank ID No. US20040010136A1 g178197
US-10-305-720-1181
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                                                                                                                           GENERAL INFORMATION:
                                                                                                                                               Sequence 31, Application US/10034650 Publication No. US20030216558A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQ ID NO 41
LENGTH: 3274
           APPLICANT: Engelhard, Eric
TITLE OF INVENTION: NOVEL COMPOSITIONS AND METHODS
TITLE OF INVENTION: CANCER
FILE REFERENCE: 529452000128
                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
                                                                                   APPLICANT: Morris, David APPLICANT: Engelhard, E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 41, Application US/10225567A
Publication No. US20030113798A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION NUMBER: 09/016,434
PRIOR FILING DATE: 1998-01-30
NUMBER OF SEQ ID NOS: 1490
SOFTWARE: PERL PROGram
SEQ ID NO 1181
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CURRENT APPLICATION NUMBER: US/10/034,650
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CURRENT APPLICATION NUMBER: US/10/225,567A
CURRENT FILING DATE: 2001-12-19
PRIOR APPLICATION NUMBER: 60/257,144
PRIOR FILING DATE: 200-12-19
NUMBER OF SEQ ID NOS: 2292
SOFTWARE: Patentin version 3.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: LifeSpan Biosciences
APPLICANT: Brown, Joseph P.
APPLICANT: Brown, Joseph P.
APPLICANT: Burmer, Glenna C.
APPLICANT: Rough, Christine L.
APPLICANT: ROugh, Christine L.
APPLICANT: ROUgh, Christine L.
ANTIGENIC PEPTIDES AND ANTIBODIES FOR G PROTEIN-COUPLED RECEPTORS
FILE REFERENCE: 1920-4-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Au-Young, Janice K.; Seilhamer, Jeffrey J.
TITLE OF INVENTION: Composition for the Detection of Signaling Pathway Gene Expression
FILE REFERENCE: PA-0002-1 CON
CURRENT APPLICATION NUMBER: US/10/305,720
CURRENT FILING DATE: 2002-11-26
                                                                                                                                                                                                                                                                                                                                                                                                                                                           ORGANISM: Homo sapiens
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                                                                                                                                                                                                                                                                  880 GAGGATGAAGCTGAAGAGGAGGAAGAAGAGGAGGAGGAAGAAGAGTGT 930
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Similarity 100.0%;
51; Conservative 0
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Pred. No. 9.4e-06;
); Mismatches 0;
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FILE REFERENCE: A116US
CURRENT APPLICATION NUMBER: US/09/972,546
CURRENT FILING DATE: 2001-10-06
PRIOR APPLICATION NUMBER: 60/238,361
PRIOR FILING DATE: 2000-10-06
NUMBER OF SEQ ID NOS: 19
SOFTWARE: PACENTIN Ver. 2.1
SEQ ID NO 16
LENGTH: 215980
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US-09-972-546-16/c
US-09-972-546-16/c
; Sequence 16, Application US/09972546
; Publication No. US20030124704A1
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; LENGTH: 68233
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-034-650-31
                                                 LOCATION: (12270). (12369)
OTHER INFORMATION: a, t, c, g
NAME/KEY: moddfied base
LOCATION: (13438). (13537)
OTHER INFORMATION: a, t, c, g
                                                                                                                          OTHER INFORMATION: a, t, c, g
NAME/KEY: modified base
LOCATION: (7481). (7580)
OTHER INFORMATION: a, t, c, g
NAME/KEY: modified base
LOCATION: (8849). (8948)
OTHER INFORMATION: a, t, c, g
NAME/KEY: modified base
LOCATION: (10375). (10474)
OTHER INFORMATION: a, t, c, g
NAME/KEY: modified base
LOCATION: (10270). (12369)
OTHER INFORMATION: a, t, c, c, g
NAME/KEY: modified base
LOCATION: (12270). (12369)
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NAME/KEY: modified base
LOCATION: (2123). (2222)
OTHER INFORMATION: a.t. c, g
NAME/KEY: modified base
LOCATION: (3728). (3927)
OTHER INFORMATION: a.t. c, g
NAME/KEY: modified base
LOCATION: (3728). (3927)
OTHER INFORMATION: a.t. c, g
OTHER INFORMATION: a.t. c, g
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PRIOR APPLICATION NUMBER: US 09/474,377
PRIOR FILING DATE: 1999-12-29
PRIOR APPLICATION NUMBER: US 09/798,586
PRIOR FILING DATE: 2001-03-02
NUMBER OF SEO ID NOS: 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: STRITTMATTER, STEPHEN APPLICANT: CATE, RICHARD L. APPLICANT: SAH, DINAH W.Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: CATE, RICHARD L.
APPLICANT: SAH, DINAH W.Y.
TITLE OF INVENTION: NOGO RECEPTOR HOMOLOGS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: FastSEQ for Windows Version 4.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: DNA
ORGANISM: Mus sp.
                                     AME/KEY: modified_base
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Local Similarity 91.7%;
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Pred. No. 0.0037;
0; Mismatches 4;
   other or unknown
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LOCATION: (68518)

OTHER INFORMATION: a, t, c, g
NAME/KEY: modified base
LOCATION: (68534)...(68633)
OTHER INFORMATION: a, t, c, g
NAME/KEY: modified base
LOCATION: (74552)...(74651)
OTHER INFORMATION: a, t, c, g
NAME/KEY: modified base
LOCATION: (814646)...(81545)
OTHER INFORMATION: a, t, c, g
NAME/KEY: modified base
LOCATION: (88519)...(88618)
OTHER INFORMATION: a, t, c, g
NAME/KEY: modified base
LOCATION: (88519)...(88618)
OTHER INFORMATION: a, t, c, g
NAME/KEY: modified base
                                                                                                                                                                                                                                                                                                                                                                                       NAME/KBY: modified base
LOCATION: (51380)..(51479)
OTHER INFORMATION: a, t, c, g
NAME/KBY: modified base
LOCATION: (56740)
OTHER INFORMATION: a, t, c, g
NAME/KBY: modified base
LOCATION: (56765)..(56864)
OTHER INFORMATION: a, t, c, g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   OTHER INFORMATION: a, t, c, g
NAME/KEY: modified base
LOCATION: (44809)...(44908)
OTHER INFORMATION: a, t, c, g
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OTHER INFORMATION: a, t, c, c)
NAME/KEY: modified base
LOCATION: (30901)...(31000)
OTHER INFORMATION: a, t, c, c)
NAME/KEY: modified base
LOCATION: (34434)...(34542)
OTHER INFORMATION: a, t, c, c)
NAME/KEY: modified base
LOCATION: (38205)...(38304)
OTHER INFORMATION: a, t, c, c)
NAME/KEY: modified base
LOCATION: (42373)
OTHER INFORMATION: a, t, c, c)
NAME/KEY: modified base
LOCATION: (42396)
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LOCATION: (18223)..(18322)
OTHER INFORMATION: a, t, c, g
NAME/KEY: modified base
LOCATION: (20974)..(21073)
OTHER INFORMATION: a, t, c, g
NAME/KEY: modified base
LOCATION: (24403)..(24502)
OTHER INFORMATION: a, t, c, g
NAME/KEY: modified base
LOCATION: (27674)..(27673)
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NAME/KEY: modified base
LOCATION: (4239)
OTHER INFORMATION: a, t, o
NAME/KEY: modified base
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LOCATION: (62818)...(62917)
OTHER INFORMATION: a, t, c,
NAME/KEY: modified base
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OTHER INFORMATION: a, t, c
NAME/KEY: modified base
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INFORMATION: a, t, KEY: modified_base
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OTHER INFORMATION: a, t, c, NAME/KEY: modified base LOCATION: (182242) . (182341) OTHER INFORMATION: a, t, c,
OTHER INFORMATION: a, t
                                                                                                                                           OTHER INFORMATION: a, t, NAME/KEY: modified base LOCATION: (164708)
                            NAME/KEY: modified base LOCATION: (192158)
                                                                                                       NAME/KEY: modified LOCATION: (164710)
                                                                                                                                                                                                                              LOCATION: (151051)
OTHER INFORMATION: a, t, c,
NAME/KEY: modified base
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OTHER INFORMATION: a, t, c, g,
NAME/KEY: modified base
(119232)
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OTHER INFORMATION: a, t, c, g
NAME/KEY: modified base
***OCATION: (12763)...(127162)
                                                                                                                                OTHER INFORMATION:
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OTHER INFORMATION: a, t,
NAME/KEY: modified base
LOCATION: (164706)
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OTHER INFORMATION: a, t, c,
NAME/KEY: modified_base
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OTHER INFORMATION: a, t, c,
NAME/KEY: modified base
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OTHER INFORMATION: a, t,
NAME/KEY: modified_base
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THER INFORMATION: a, t,

NAME/KEY: modified_base
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OTHER INFORMATION: a, t,
NAME/KEY: modified base
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LOCATION: (96570). (96573)
OTHER INFORMATION: a, t, c,
NAME/KEY: modified base
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OTHER INFORMATION: a, t,
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LOCATION: (96666)
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/KEY: modified base
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; LCCATION: (1)...(1341)
; OTHER INFORMATION: Coding sequence for variant human
; OTHER INFORMATION: alpha-2B-adrenoceptor protein
US-09-825-923-1
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                                                                                                                                                      US-10-077-870-1
Sequence 1, Application US/10077870
Publication No. US20030003470A1
GENERAL INFORMATION:
APPLICANT: Salonen, Jukka T
TITLE OF INVENTION: Method for detecting a
FILE REFERENCE: 093-0183P
CURRENT APPLICATION NUMBER: US/10/077,870
CURRENT FILING DATE: 2002-05-21
                                                                                                                                                                                                                                                                                                    Query Match
Best Local S
Matches 42
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APPLICANT: Laka, Timo A
APPLICANT: Salonen, Kristiina
APPLICANT: Salonen, Riitta
APPLICANT: Kauhanen, Jussi
APPLICANT: Valkonen, Veli-Pekka
APPLICANT: Valkonen, Veli-Pekka
TITLE OF INVENTION: A DNA molecule encoding a variant alpha-2B-adrenoceptor
TITLE OF INVENTION: protein, and uses thereof
TITLE REFERENCE: Alpha-2B-AR variant
CURRENT APPLICATION NUMBER: US/09/825,923
CURRENT FILING DATE: 2001-04-05
CURRENT FILING DATE: 2001-04-05
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Patent No. US20010016338A1
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PRIOR FILING DATE: 2000-05-25
NUMBER OF SEQ ID NOS: 10
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APPLICANT: Heinonen, Pe
APPLICANT: Alhopuro, Pi
APPLICANT: Karvonen, Ma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH: 1344
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
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                                                                                                                                                                                                                                                                                               Similarity 93.3
42; Conservative
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Pesonen, Ullamari
Scheinin, Mika
Salonen, Jukka T
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Alhopuro, Pia
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91.7%;
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Pred. No. 0.00:
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                                                of hypertension and uses thereof
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US-09-728-446-1420/c
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US-09-728-444-146
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                                                                                                                                                                     Sequence 1420, Application US/09728446
Patent No. US20020081668A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
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SEQ ID NO 146
LENGTH: 223
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Patent No. US20020161207A1
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                APPLICANT: Friedrich, Glenn
APPLICANT: Zambrowicz, Brian
APPLICANT: Sands, Arthur T.
APPLICANT: Sands, Arthur T.
TITLE OF INVENTION: No. US20020081668A1el Murine Polynucleotide Sequences
TITLE OF INVENTION: and Mutant Cells and Mutant Animals Defined Thereby
FILE REFERENCE: LEX-0101-USA
CURRENT APPLICATION NUMBER: US/09/728,446
CURRENT FILING DATE: 2000-11-30
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APPLICANT: Sands, Arthur T.
TITLE OF INVENTION: NO. US20020161207A1el Murine Polynucleotide Sequences
TITLE OF INVENTION: and Mutant Cells and Mutant Animals Defined Thereby
FILE REFERENCE: LEX-0100-USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CURRENT APPLICATION NUMBER: US/09/728,444
CURRENT FILING DATE: 2000-11-30
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PRIOR APPLICATION NUMBER: US 60/168,270
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NAME/KEY: CDS
LOCATION: (1)..(1341)
OTHER INFORMATION: Coding sequence for variant human alpha-2B-adrenoceptor protein
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NAME/KEY: misc_feature

LOCATION: (1)...(223)

OTHER INFORMATION: n = A,T,C or G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: DNA
ORGANISM: Mus musculus
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ORGANISM: Homo sapiens
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les 43; Conserv
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Local Similarity 93.3%;
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                                                                                                                                                                                                                                                                                                                  Conservative
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Pred. No. 0.013;
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US-10-425-114-10213
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APPLICANT: Sands, Arthur T.

PPLICANT: Sands, Arthur T.

ITTLE OF INVENTION: No. US20020161207A1el Murine Polynucleotide Sequences
TITLE OF INVENTION: and Mutant Cells and Mutant Animals Defined Thereby
FILE REFERENCE: LEX-0100-USA
CURRENT APPLICATION NUMBER: US/09/728,444
CURRENT FILING DATE: 2000-11-30
PRIOR APPLICATION NUMBER: US 60/168,360
PRIOR FILING DATE: 1999-12-01
NUMBER OF SEQ ID NOS: 1206
SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQ ID NOS: 1461
SOFTWARE: FastSEQ for Windows
SEQ ID NO 1420
                                                                                                                                                                                    GENERAL INFORMATION:
                                                                                                                                                                                                        Sequence 10213, Application US/10425114 Publication No. US20040034888A1
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Best Local :
                                                                      APPLICANT:
APPLICANT:
APPLICANT:
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                 APPLICANT: Kovalic, David K.
APPLICANT: Screen, Steven E
APPLICANT: Tabaska, Jack E
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(53313)B
                                                                                                                                 APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Friedrich, Glenn
APPLICANT: Zambrowicz, Brii
APPLICANT: Sands, Arthur T
                                                                                                                                                                 APPLICANT: Liu, Jingdong
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FEATURE:
FEATURE:
LOCATION: (1)...(234)
OTHER INFORMATION: n = A,T,C
CURRENT APPLICATION NUMBER: US/10/425,114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME/KEY: misc_feature LOCATION: (1)...(330)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: DNA
ORGANISM: Mus musculus
FEATURE:
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Local Similarity 89.6%;
les 43; Conservation
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Local Similarity 89.6%;
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Pred. No. 0.013;
0; Mismatches
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Pred. No. 0.013;
0; Mismatches
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FEATURE: Clone ID: 700899387_FLI
OTHER INFORMATION: Clone ID: 700899387_FLI
OTHER 114-10213
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CURRENT FILING ID NOS: 7:
NUMBER OF SEQ ID NOS: 10:013
SEQ ID NO 10213
LENGTH: 642
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US-10-161-927-81
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Query Match
Best Local Similarity 89.6%;
Best Local Similarity
Matches 43; Conservative
                                                                                                                                   PRIOR FILING DATE: 2001-06-12
PRIOR FILING DATE: 2001-06-12
PRIOR APPLICATION NUMBER: 60/259,685
PRIOR FILING DATE: 2001-09-27
PRIOR APPLICATION NUMBER: 60/299,133
PRIOR FILING DATE: 2001-06-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PPLICANT: SCURE DAVID J.

THE OF INVENTION: NOVEL HUMAN PROTEINS, POLYNUCLEOTIDES ENCODING THEM AND METHODS.

ITLE OF INVENTION: THE SAME 677 OCHER)

THE SETERENCE: 21402-377 D (CUIA 677 OCHER)

THE REFERENCE: 21402-377 D (CUIA 677 OCHER)

THERENT DESCRIPTION NUMBER: US/10/161,927
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PRIOR PELICATION NUMBER: 60/296,575
PRIOR PILING DATE: 2001-06-07,414
PRIOR APPLICATION NUMBER: 60/297,414
PRIOR APPLICATION NUMBER: 60/297,819
PRIOR FILING DATE: 2001-06-11,
PRIOR FILING DATE: 2001-06-11,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 GAGGATGAAGCTGAAGAGGAGGAGGAGGAGGAGGAGGAGGAAGAAGA 48
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TOR APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RRENT FILING DATE: 2002-06-03, 661
                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION NUMBER: 60/297,567
Remaining prior Application data removed - See File Wrapper or PALM.

Remaining Prior Application data removed - See File Wrapper or PALM.

Remaining Prior Application data removed - See File Wrapper or PALM.

REMOTE DIVERSE DIVER
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TOR APPLICATION NUMBER: 60/296,418
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No. US20030235821A1
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Baumgartner, Jason C.
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114 Esha A.
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pred, No. 0.012;
pred, No. mismatches .
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FEATURE:
FEATURE:
NAME/KEY: CDS
LOCATION: (26)...(1166)
100-10-161-927-81
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FILE REFERENCE: 20402-377 D (Cura 677 Other)

FILE REFERENCE: 2002-06-03

CURRENT PILING DATE: 2002-06-03

CURRENT PILING DATE: 2001-06-06

PRIOR APPLICATION NUMBER: 60/295,667

PRIOR APPLICATION NUMBER: 60/295,607

PRIOR APPLICATION NUMBER: 60/295,404

PRIOR FILING DATE: 2001-06-06

PRIOR PILING DATE: 2001-06-06

PRIOR PILIN
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publication No. US20030235821A1
                                                                                                                                                                                                                                                                                                                                                                                                                     Remaining Prior Application data removed - See File Wrapper or PALM.

Remaining Prior Application data removed - See File Wrapper or PALM.

Remaining Prior Application data removed - See File Wrapper or PALM.

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PEATURE: CDS
NAME/KEY: CDS
LOCATION: (1)..(1141)
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ingolli, Esha A.
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pred. No. 0.012;
pred. No. 0.012;
o; Mismatches
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Database
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Maximum Match 100%
Listing first 45 s
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Maximum DB seq length: 200000000
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Perfect score:
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Gapop 10.0 , Gapext 1.0
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US-09-692-077D-1_COPY_880_930
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l: /cgn2_6/ptodata/2/pna/PCTUS_
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Copyright (c) 1993 - 2004 Compugen Ltd
                                                            'cgn2_6/ptodata/2/pna/US082_COMB.seq:*

'cgn2_6/ptodata/2/pna/US083_COMB.seq:*

'cgn2_6/ptodata/2/pna/US083_COMB.seq:*

'cgn2_6/ptodata/2/pna/US085_COMB.seq:*

'cgn2_6/ptodata/2/pna/US085_COMB.seq:*

'cgn2_6/ptodata/2/pna/US085_COMB.seq:*

'cgn2_6/ptodata/2/pna/US085_COMB.seq:*

'cgn2_6/ptodata/2/pna/US085_COMB.seq:*

'cgn2_6/ptodata/2/pna/US090_COMB.seq:*

'cgn2_6/ptodata/2/pna/US091_COMB.seq:*

'cgn2_6/ptodata/2/pna/US093A_COMB.seq:*

'cgn2_6/ptodata/2/pna/US093B_COMB.seq:*

'cgn2_6/ptodata/2/pna/US093B_COMB.seq:*

'cgn2_6/ptodata/2/pna/US093B_COMB.seq:*

'cgn2_6/ptodata/2/pna/US093B_COMB.seq:*

'cgn2_6/ptodata/2/pna/US095B_COMB.seq:*

'cgn2_6/ptodata/2/pna/US095B_COMB.seq:*

'cgn2_6/ptodata/2/pna/US095B_COMB.seq:*

'cgn2_6/ptodata/2/pna/US095B_COMB.seq:*

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'cgn2_6/ptodata/2/pna/US096B_COMB.seq:*

'cgn2_6/ptodata/2/pna/US096B_COMB.seq:*

'cgn2_6/ptodata/2/pna/US097B_COMB.seq:*

'cgn2_6/ptodata/2/pna/US097B_COMB.seq:*

'cgn2_6/ptodata/2/pna/US098B_COMB.seq:*

'cgn2_6/ptodata/2/pna/US099B_COMB.seq:*

'cgn2_6/ptodata/2/pna/US099B_COMB.seq:*

'cgn2_6/ptodata/2/pna/US099B_COMB.seq:*
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44. /cgm2_6/ptodata/2/pna/USI010 COMB. seq:
46. /cgm2_6/ptodata/2/pna/USI011A_COMB. seq:
46. /cgm2_6/ptodata/2/pna/USI011A_COMB. seq:
46. /cgm2_6/ptodata/2/pna/USI01B_COMB. seq:
49. /cgm2_6/ptodata/2/pna/USI01B_COMB. seq:
50. /cgm2_6/ptodata/2/pna/USI01B_COMB. seq:
51. /cgm2_6/ptodata/2/pna/USI01B_COMB. seq:
52. /cgm2_6/ptodata/2/pna/USI01B_COMB. seq:
53. /cgm2_6/ptodata/2/pna/USI01B_COMB. seq:
53. /cgm2_6/ptodata/2/pna/USI01B_COMB. seq:
53. /cgm2_6/ptodata/2/pna/USI01C_COMB. seq:
53. /cgm2_6/ptodata/2/pna/USI01C_COMB. seq:
53. /cgm2_6/ptodata/2/pna/USI01C_COMB. seq:
53. /cgm2_6/ptodata/2/pna/USI01C_COMB. seq:
53. /cgm2_6/ptodata/2/pna/USI001C_COMB. seq:
53. /cgm2_6/ptodata/2/pna/USI001C_COMB. seq:
53. /cgm2_6/ptodata/2/pna/USI001C_COMB. seq:
53. /cgm2_6/ptodata/2/pna/USI001C_COMB. seq:
54. /cgm2_6/ptodata/2/pna/USI001C_COMB. seq:
55. /cgm2_6/ptodata/2/pna/USI001C_COMB. seq:
56. /cgm2_6/ptodata/2/pna/USI001C_COMB. seq:
57. /cgm2_6/ptodata/2/pna/USI001C_COMB. seq:
58. /cgm2_6/ptodata/2/pna/USI001C_COMB. seq:
59. /cgm2_6/ptodata/2/pna/USI001C
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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Sequence 24, Application US/09692077D
GENERAL INFORMATION:
APPLICANT: Liggett, Stephen
APPLICANT: Small, Kersten M.
TITLE OF INVENTION: Alpha-2B-Adrenergic Receptor Polymorphisms
FILE REFERENCE: 10738-43
CURRENT APPLICATION NUMBER: US/09/692,077D
CURRENT FILING DATE: 2000-10-19
NUMBER OF SEQ ID NOS: 26
SOFTWARE: PatentIn version 3.2
LENGTH: 69
Type: DNA
ORGANISM: Homo sapiens
US-09-692-077D-24
                                                                                                                                                                                                                                                    RESULT 1
US-09-692-077D-24
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No.
      Query Match
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US-60-207-360-110
US-60-207-360-112
US-60-207-360-113
US-60-207-360-113
US-60-207-360-115
US-60-207-360-115
US-60-207-360-116
US-60-207-360-118
US-60-207-307-308
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2 US-60-453-050-6437
2 US-60-453-135-6437
3 US-60-466-412-6437
US-09-949-004-175
US-10-305-720-1181
US-10-225-567A-41
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US-09-692-077B-1

US-09-692-077D-1

US-09-692-077D-1

US-09-825-923-3

US-10-001-073-1

US-10-001-073A-1
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US-10-001-073A-54

US-60-164-763-274

US-60-169-842-1935

US-60-170-346-61

US-09-726-174-3537

US-60-160-189-1492

US-60-160-190-231
   Score 51;
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US-60-169-841-1172
US-60-169-842-2193
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   B
 29;
Length
                                                                                                                                                                                                                                                                                                                                                                                    Sequence 24, Appl Sequence 27, Appl Sequence 274, Appl Sequence 11, Appl Sequence 61, Appl Sequence 231, Appl Sequence 231, Appl Sequence 231, Appl Sequence 3537, App Sequence 3708, App Sequence 3151, App Sequence 3, Appli Sequence 1, Appli Sequence 1, Appli Sequence 3, Appli Sequence 3, Appli Sequence 1, Appli Sequence 1, Appli Sequence 6437, App Sequence 6437, App Sequence 6437, App Sequence 1181, App Sequence 1181, App Sequence 111, App Sequence 112, App Sequence 113, App Sequence 114, App Sequence 114, App Sequence 117, App Sequence 117, App Sequence 111, App Sequence 112, App Sequence 113, App Sequence 114, App Sequence 114, App Sequence 115, App Sequence 116, App Sequence 116, App Sequence 117, App Sequence 117, App Sequence 118, App 
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Matches 51
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TYPE: DNA
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Sequence 54, Application US/10001073A
GENERAL INFORMATION:
APPLICANT: Small, Kersten M.
APPLICANT: Small, Kersten M.
APPLICANT: Liggett, Stephen
TITLE OF INVENTION: Alpha-2 Adrenergic Receptor Polymorphisms
FILE REFERENCE: 10738-42
CURRENT APPLICATION NUMBER: US/10/001,073A
CURRENT FILING DATE: 2001-11-01
NUMBER OF SEQ ID NOS: 69
SOFTWARE: PatentIn version 3.2
SEQ ID NO 54
LENGTH: 69
TYPE: DNA
ORGANISM: Homo sapiens
US-10-001-073A-54
                                                                                                                                                           US-60-169-842-1935/c
                                                                                                                                                                                                                                                                                                                                                              ; ORGANISM: Human
US-60-164-763-274
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US-60-164-763-274/c
Sequence 274, Application US/60164763; GENERAL INFORMATION:
Sequence 1935, Application US/60169842

GENERAL INFORMATION:
APPLICANT: Bonazzi, Vivien
TITLE OF INVENTION: ISOLATED HUMAN GPCR PROTEIN, NUCLEIC
TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN GPCR PROTEINS AND USES THEREOF
FILE REFERENCE: CLOO0162
CURRENT APPLICATION NUMBER: US/60/169,842
CURRENT FILING DATE: 1999-12-09
NUMBER OF SEQ ID NOS: 5232
                                                                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQ ID NOS: 1154
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 274
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TITLE OF INVENTION: ISOLATED HUMAN GPCR PROTEIN, NUCLEIC
TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN GPCR PROTEINS AND USES THEREOF
FILE REFERENCE: CL000140
CURRENT APPLICATION NUMBER: US/60/164,763
CURRENT FILING DATE: 1999-11-12
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100.0%; Pred. No. 0.15;
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Pred. No. 0.14;
Mismatches
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; NAME/KEY: misc_feature
; LOCATION: (1)...(516)
; OTHER INFORMATION: n = A,T,C or G
US-09-726-174-3537
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SEQ ID NO 3537
LENGTH: 516
TYPE: DNA
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GENERAL INFORMATION:
APPLICANT: BONRZZI, VIVIEN
TITLE OF INVENTION: ISOLATED HUMAN GPCR PROTEIN, NUCLEIC
TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN GPCR PROTEINS AND USES THEREOF
FILE REFERENCE: CL000147
CURRENT APPLICATION NUMBER: US/60/170,346
CURRENT FILING DATE: 1999-12-13
NUMBER OF SEQ ID NOS: 2600
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 61
LENGTH: 481
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SEQ ID NO 1935
LENGTH: 481
                                     Matches
                                                     Query Match
Best Local Similarity
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CURRENT APPLICATION NUMBER: US/09/726,174
CURRENT FILING DATE: 2000-11-29
PRIOR APPLICATION NUMBER: 60/167,857
PRIOR PILING DATE: 1999-11-29
NUMBER OF SEQ ID NOS: 5942
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-60-169-842-1935
                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Holtzman, Douglas A.
TITLE OF INVENTION: NOVEL NUCLEIC ACID MOLECULES AND USES
TITLE OF INVENTION: THEREFOR
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es 51; Conservative
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                                     51;
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GAGGATGAAGCTGAAGAGGAGGAAGAGGAGGAGGAGGAGGAAGAGTGT 51
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gearing, David P
                                 100.0%; Score 51; DB 31; ilarity 100.0%; Pred. No. 0.14; Conservative 0; Mismatches 0;
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100.0%; Pred. No. 0.1
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Pred. No. 0.14;
0; Mismatches
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                                                                     Length 516;
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                                   Indels
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                                   Gaps
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; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 231
; LENGTH: 569
; TYPE: DNA
; ORGANISM: HUMAN
US-60-160-190-231
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; ORGANISM: HUMAN
US-60-160-189-1492
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                                                                                                                                                                                                                RESULT 9
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                                                                                                                                                                                            US-60-160-202-659
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                                                                                                                                                   Sequence 659, Application US/60160202
GENERAL INFORMATION:
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Best Local Similarity
APPLICANT: BONAZZI, VIVIEN
TITLE OF INVENTION: ISOLATED HUMAN GPCR PROTEIN, N
TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN
FILE REFERENCE: CL000114
CURRENT APPLICATION NUMBER: US/60/160,202
CURRENT FILING DATE: 1999-10-19
NUMBER OF SEQ ID NOS: 4392
SOFTWARE: FastSEQ for Windows Version 4.0
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TITLE OF INVENTION: ISOLATED HUMAN DRUG TARGET PROTEINS,
TITLE OF INVENTION: WUCLEIC ACID MOLECULES ENCODING HUMAN DRUG TARGET PROTEINS
TITLE OF INVENTION: AND USES THEREOF
FILE REFERENCE: CL000112
CURRENT APPLICATION NUMBER: US/60/160,189
CURRENT FILLING DATE: 1999-10-19
CURRENT FILLING DATE: 1999-10-19
CURRENT FILLING DATE: 1999-10-19
CURRENT FILLING DATE: 1999-10-19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILE REFERENCE: CL000115
CURRENT APPLICATION NUMBER: US/60/160,190
CURRENT FILING DATE: 1998-10-19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQ ID NOS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TITLE OF INVENTION: ISOLATED HUMAN INTITLE OF INVENTION: NUCLEIC ACID MOLTITLE OF INVENTION: AND USES THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ENGTH: 569
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         51; Conservative
                                                                                                                                                                                                                                                                                                                                                                 Similarity
                                                                                                                                                                                                                                                                        GAGGATGAAGCTGAAGAGGAGGAAGAAGAGGAGGAGGAGGAGGAAGAGTGT
                                                                                                                                                                                                                                                                                                GAGGATGAAGCTGAAGAGGAGGAGGAGGAGGAGGAGGAGGAGAGAGTGT 51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              BONAZZI,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      100.0%; illarity 100.0%; Conservative 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ISOLATED HUMAN ION CHANNEL PROTEINS, NUCLEIC ACID MOLECULES ENCODING HUMAN ION CHANNEL PROTEINS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                VIVIEN
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Pred. No. 0.14;
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Pred. No. 0.14;
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                                                                                                                     NUCLEIC
                                                                                                 GPCR
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                                                                                                 PROTEINS AND USES THEREOF
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CURRENT APPLICATION NUMBER: US/60/169,841
CURRENT FILING DATE: 1999-12-09
NUMBER OF SEQ ID NOS: 2910
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 1172
LENGTH: 569
TYPE: DNA
ORGANISM: Human
US-60-169-841-1172
RESULT 12
US-60-169-842-2193
; Sequence 2193, A
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Sequence 1172, Application US/60169841

GENERAL INFORMATION:

APPLICANT: Bonazzi, Vivien

TITLE OF INVENTION: ISOLATED HUMAN ION CHANNEL PROTEINS,

TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN ION CHANNEL PROTEINS

TITLE OF INVENTION: AND USES THEREOF

FILE REFERENCE: CL000163
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; ORGANISM: Human
US-60-169-840-3708
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US-60-169-840-3708
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                                                                                                                                                        Matches
                                                                                                                                                                                            Query Match
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TITLE OF INVENTION: ISOLATED HUMAN SECRETED PROTEINS,
TITLE OF INVENTION: UNCLEIC ACID MOLECULES ENCODING HUMAN SECRETED PROTEINS
TITLE OF INVENTION: USES THEREOF
FILE REFERENCE: CL000164
CURRENT FILIG DATE: 1999-12-09
NUMBER OF SEQ ID NOS: 9628
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 3708
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: DNA
                                                                                                                                                                        Local Similarity
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es 51; Conservative
                                                                                      24
                                                                                                                                                         51;
                                                                                                   1 GAGGATGAAGCTGAAGAGGAGGAAGAAGAGGAGGAGGAGGAGGAGGAAGAGTGT 51
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    51; Conservative
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                                                                               GAGGATGAAGCTGAAGAGGAGGAAGAGGAGGAGGAAGAAGAGTGT
                                                                                                                                              100.0%; Score 51; DB 72; Length 569; ilarity 100.0%; Pred. No. 0.14; Conservative 0; Mismatches 0; Indels
Application US/60169842
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Pred. No. 0.14;
0; Mismatches
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GENERAL INFORMATION:
APPLICANT: Bonazzi, Vivien
ITILE OF INVENTION: ISOLATED HUMAN GPCR PROTEIN, NUCLEIC
ITILE OF INVENTION: ACID MOLECULES ENCODING HUMAN GPCR PROTE
FILE REFERENCE: CL000162
CURRENT APPLICATION NUMBER: US/60/169,842
UMBER OF SEQ ID NOS: 5232
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 2193
LEGTH: 569
TYPE: DNA
ORGANISM: Human
US-60-169-842-2193
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US-09-422-985-3
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; ORGANISM: Human
US-60-169-867-3351
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CURRENT FILING DATE: 1999-12-09
NUMBER OF SEQ ID NOS: 8230
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 3351
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 3351, Application US/60169867
GENERAL INFORMATION:
APPLICANT: Bonazzi, Vivien
TITLE OF INVENTION: ISOLATED HUMAN DRUG TARGET PROTEINS,
TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN DRUG TARGET PROTEINS,
TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN DRUG TARGET PROTEINS,
TITLE OF INVENTION: AND USES THEREOF
FILE REFERENCE: CL000160
                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                      Sequence 3
APPLICANT: Tuomainen, Tomi-Pekka
APPLICANT: Lakka, Timo A
APPLICANT: Nyyss"nen, Kristiina
APPLICANT: Salonen, Ritta
APPLICANT: Salonen, Jussi
APPLICANT: Valkonen, Vell-Pekka
TITLE OF INVENTION: A DNA molecule encoding a variant alpha-2B-adrenoceptor
TITLE OF INVENTION: protein, and uses thereof
FILE REFERENCE: Alpha-2B-AR variant
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APPLICANT:
APPLICANT:
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Best Local
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nes 51; Conservative
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Alhopuro, Pia
Karvonen, Matti
Koulu, Markku
Pesonen, Ullamari
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                                                                                                                                                                                                                                                                                                                                                  Application US/09422985
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                                                                                                                                                                           Scheinin, Mika
Salonen, Jukka T
                                                                                                                                                                                                                                                                                                                Snapir, Amir
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Pred. No. 0.14;
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CURRENT APPLICATION NUMBER: US/09/422,985
CURRENT FILING DATE: 1999-10-22
NUMBER OF SEQ ID NOS: 10
SOFTWARE: Pacentin Ver. 2.1
SEQ ID NO 3
LENGTH: 1353
TYPE: DNA
ORGANISM: Homo Bapiens
PEATURE:
NAME/KEY: CDS
LOCATION: (1). (1350)
OTHER INFORMATION: Coding sequence for human alpha-2B-adrenoceptor
US-09-422-985-3
                                                                                                                                                                                                                                                             FILE REFERENCE: Sequences 1-22
CURRENT APPLICATION NUMBER: US/99/692,077B
CURRENT FILING DATE: 2000-10-19
NUMBER OF SEQ ID NOS: 22
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 1
LENGTH: 1353
TYPE: DNA
ORGANISM: Homo sapiens
US-09-692-077B-1
                                                                                                                        5
                                                                                      밁
Search completed: March 2, 2004, 11:49:23 Job time : 2893 secs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 15
US-09-692-077B-1
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                                                                                                                                                                    Query Match 100.0%; Score 51; DB 29; Length 1353; Best Local Similarity 100.0%; Pred. No. 0.13; Matches 51; Conservative 0; Mismatches 0; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 1, Application US/09692077B GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 100.0%; Score 51; DB 20; Length 1353; Best Local Similarity 100.0%; Pred. No. 0.13; Matches 51; Conservative 0; Mismatches 0; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Liggett, Stephen
TITLE OF INVENTION: Alpha-2B-adrenergic receptor polymorphisms
                                                                                    880 GAGGATGAAGAGAGGAGGAAGAGGAGGAGGAAGAAGAGTGT 930
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              880 GAGGATGAAGCTGAAGAGGAGGAAGAGGAGGAGGAGGAAGAGTGT 930
                                                                                                             1 GAGGATGAAGCTGAAGAGGAGGAGGAGGAGGAGGAGGAGGAGAGAGTGT 51
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Title:
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB
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    Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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             34.35
34.25
34.24
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seq length:
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                                                                                                                                                                                                                                                                                                                    Query
Match Length
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Gapop 10.0 , Gapext 1.0
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1: /cgn2_6/ptodata/1/pna/PCT_NEW_COMB.seq:*

2: /cgn2_6/ptodata/1/pna/US06_NEW_COMB.seq:*

3: /cgn2_6/ptodata/1/pna/US07_NEW_COMB.seq:*

4: /cgn2_6/ptodata/1/pna/US08_NEW_COMB.seq:*

5: /cgn2_6/ptodata/1/pna/US08_NEW_COMB.seq:*

6: /cgn2_6/ptodata/1/pna/US09_NEW_COMB.seq:*

7: /cgn2_6/ptodata/1/pna/US09_NEW_COMB.seq:*
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5.3 188053
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US-10-451-467A-261
US-10-417-375A-167
US-10-417-375A-167
US-10-417-375A-125
PCT-US04-02188-20
US-10-64-425-20
US-10-64-425-20
US-10-64-25-66
PCT-US03-32805-1
US-10-767-701-2420
US-10-767-701-26619
US-10-767-701-15708
US-10-767-701-15708
US-10-767-701-15708
US-10-767-701-15708
US-10-767-701-15708
US-10-767-701-15709
US-10-767-701-15709
US-10-767-701-15709
US-10-767-701-15500
US-10-767-701-23701
US-10-767-701-23701
US-10-767-471-10616
US-10-767-701-375A-15
US-10-767-471-375A-15
US-10-767-471-10616
US-10-767-471-375A-15
US-10-767-471-31517
                                                                                                                                                                                                                                                                                                                                                        SUMMARIES
                                                                                         Sequence 1, Appli
Sequence 24209, A
Sequence 10555, A
Sequence 79, Appl
Sequence 63, Appl
Sequence 26619, A
Sequence 15708, A
Sequence 10125, A
Sequence 14827, A
Sequence 7, Appli
            Sequence 1, Appli
Sequence 15, Appl
Sequence 23701, A
Sequence 10616, A
Sequence 31476, A
Sequence 375, App
                                                                                                                                                                                             Sequence 167, App
Sequence 125, App
Sequence 20, Appl
Sequence 20, Appli
Sequence 6, Appli
Sequence 1, Appli
Sequence 1, Appli
                                                                                                                                                                                                                                                                                                                     Description
                                                                                                                                                                                                                                                                               Sequence 261, App
Sequence 79, Appl
                                                                               Sequence
                                                                              7, Appli
9500, Ap
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27 34.2 67.1 803755 6 US-10-767-471-10700 29 33.8 66.3 2525 6 US-10-767-471-10700 29 33.8 66.3 2525 6 US-10-770-726-5 20 31 33.6 65.9 201 6 US-10-767-471-39939 20 31 33.6 65.9 201 6 US-10-767-471-39939 21 33.6 65.9 201 6 US-10-767-471-39942 23 33.6 65.9 201 6 US-10-767-471-39942 24 33.6 65.9 201 6 US-10-767-471-39942 25 34 33.6 65.9 201 6 US-10-767-471-39942 26 35 33.6 65.9 201 6 US-10-767-471-10794 27 38 33.6 65.9 1316 6 US-10-767-471-10794 38 33.6 65.9 186191 6 US-10-767-471-7934 39 33.6 65.9 186191 6 US-10-767-471-7934 41 33.2 65.1 201 6 US-10-767-471-7934 42 33.2 65.1 201 6 US-10-767-471-7957 43 33.2 65.1 201 6 US-10-767-471-7957 44 33.2 65.1 3129 6 US-10-767-471-30298 45 33.2 65.1 3129 6 US-10-767-471-422							_	_	_	_	_	_	_	_	_	_		_	
2 67.1 803755 6 US 8 66.3 2525 6 US 6 65.9 201 6 US 6 65.9 201 6 US 6 65.9 201 6 US 6 65.9 35895 6 US 6 65.9 35895 6 US 6 65.9 35895 6 US 6 65.9 186191 6 US 6 6 6 6 6 6 5 US 6 6 6 6 6 6 5 US 6 6 6 6 6 5 US 6 6 6 6 6 US 6 6 6 6 US 6 6 6 6 US 6 6 6 US 6 6 6 US 6 6 6 US 6 US	45	44	43	42	41	40											29		
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	US-10-767-471-422	US-10-767-471-423	US-10-767-471-30298	US-10-767-471-7957	US-10-767-471-7946	US-10-767-471-7934	'US-10-767-471-10794	US-10-765-790-72	US-10-767-471-10749	US-10-767-701-13537	US-10-767-701-11656	US-10-767-471-39944	US-10-767-471-39942	US-10-767-471-39939	US-10-767-471-39937	٠.	US-10-770-726-5	US-10-767-471-10700	١
	422, App	423, App	30298, A	7957, Ap	7946, Ap	7934, Ap	10794, A	72, Appl	10749, A	13537, A	11656, A	39944, A	39942, A	39939, A	39937, A	10632, A	5, Appli	10700, A	TOTAC, W

## ALIGNMENTS

```
Sequence 79, Application US/10417375A
GENERAL INFORMATION:
APPLICANT: David W. Morris
APPLICANT: Marc Malandro
ITITLE OF INVENTION: Novel Therapeutic Targets in
FILE REFERENCE: 529452001600
CURRENT APPLICATION NUMBER: US/10/417,375A
CURRENT FILING DATE: 2003-04-15
NUMBER OF SEQ ID NOS: 176
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION NUMBER: EP 00870318.3
PRIOR FILING DATE: 2000-12-22
PRIOR APPLICATION NUMBER: EP 01870002.1
PRIOR EILING DATE: 2001-01-04
PRIOR APPLICATION NUMBER: EP 01870003.9
PRIOR FILING DATE: 2001-01-09
PRIOR FILING DATE: 2001-01-09
NUMBER OF SEQ ID NOS: 732
SOFTWARE: PATENTIN VERSION 3.1
SEQ ID NO 261
LENGTH: 1721
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; TYPE: DNAy; ORGANISM: Saccharomyces cerevisiae US-10-451-467A-261
                                                                                                                                                                                                                                                                                                RESULT 2
US-10-417-375A-79/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; Sequence 261, Application US/10451467A GENERAL INFORMATION: APPLICANT: CONTRERAS, ROLAND HENRI APPLICANT: EBERHARDT, INES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-10-451-467A-261/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 79.6%; Score 40.6; DB 6; Length 1721; Best Local Similarity 91.5%; Pred. No. 0.0039; Matches 4; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: LUYTEN, WALTER HERMAN MARIA LOUIS
APPLICANT: REEKMANS, RIEKA JOSEPHINA
TITLE OF INVENTION: BAX-RESPONSIVE GENES FOR DRUG TARGET IDENTIFICATION IN
TITLE OF INVENTION: YEAST AND FUNGI
FILE REFERENCE: JAB-1667
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CURRENT FILING DATE: 2003-06-19
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; LENGTH: 54303 ; TYPE: DNA ; ORGANISM: Mus musculus US-10-417-375A-79

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NAME/KEY: misc_feature
LOCATION: (1)...(188053)
OTHER INFORMATION: n = A,T,C or G
                                     Query Match
Best Local Similarity 87.5
42; Conservative
                                                                                                                                                                                                                                                           RESULA .
US-10-417-375A-125
. Sequence 125, Application US/10417375A
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                                                                                                                                                                  SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                             ORGANISM: Mus musculus FEATURE:
                                                                                                                                                                                                                APPLICANT: David W. Morris
APPLICANT: Marc Malandro
TITLE OF INVENTION: Novel Therapeutic Targets
FILE REFERENCE: 529452001600
                                                                                                                                                                                           NUMBER OF SEQ ID NOS:
                                                                                                                                                                                                     CURRENT APPLICATION NUMBER: CURRENT FILING DATE: 2003-(
                                                                                                                                                                                                                                                                                                                                                                              Matches
                                                                                                                                                          TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                  NAME KEY: misc_feature
LOCATION: (1)...(150085)
OTHER INFORMATION: n = A,T,C or G
                                                                                                                                                                                                                                                                                                              Local
1 GAGGATGAAGCTGAAGAGGAGGAGGAAGAGGAGGAGGAAGAGTG 50
                                                                                                                                                                                                                                                                                                                                                                             43;
                                                                                                                                                                                                                                                                                                                                                                     Similarity 86.0
43; Conservative
                                    75.3%; Score 38.4; DB 6;
87.5%; Pred. No. 0.02;
7ative 0; Mismatches 6;
                                                                                                                                                                                                     2003-04-15
                                                                                                                                                                                                                                                                                                                                                                             76.1%;
86.0%;
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Pred. No. 0.016;
0; Mismatches 7;
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                                                  Length 188053;
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RESULT 7
US-10-642-946-6
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 Sequence 6, Application US/10642946
GENERAL INFORMATION:
APPLICANT: Ryan, James M.
TITLE OF INVENTION: Genomic Polynucleotide Fragments From Chromosome 7
FILE REFERENCE: JR-14,000-US
                                                                                                                                                                                                                                   LENGTH: 3994

LENGTH: 3994

TYPE: DNA

ORGANISM: Homo sapiens
US-10-764-425-20
                                                                                                                                                                                                                                                                       SOFTWARE: Patem
SEQ ID NO 20
TRUGTH: 3994
CURRENT APPLICATION NUMBER: US/10/642,946
                                                                                                                                                                                         Query Match
Best Local Similarity 87.2%;
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APPLICANT: Evele
APPLICANT: Bigwo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LENGTH: 3994
TYPE: DNA
ORGANISM: Homo sapiens
PCT-US04-02188-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 20, Application US/10764425 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION NUMBER: 60/442,582
PRIOR FILING DATE: 2003-01-24
NUMBER OF SEQ ID NOS: 191
                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Bigwood, Douglas
APPLICANT: Taylor, Ian
TITLE OF INVENTION: EXPRESSION PROFILES FOR COLON CANCER AND METHODS OF USE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence
                                                                                                                                                                                                                                                                                                                                         CURRENT APPLICATION NUMBER: US/10/764,425
CURRENT FILING DATE: 2004-01-23
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CURRENT APPLICATION NUMBER: PCT/US04/02188
CURRENT TALING DATE: 2004-01-23
PRIOR APPLICATION NUMBER: 60/442,582
NUMBER OF SEQ ID NOS: 191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Eveleigh, Deepa
APPLICANT: Bigwood, Douglas
APPLICANT: Taylor, Ian
TITLE OF INVENTION; EXPRESSION PROFILES FOR COLON CANCER AND METHODS OF USE
                                                                                                                 41;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity es 41; Conserv
                                                                                                                                   PatentIn version 3.2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 GAGGATGAAGCTGAAGAGGAGGAGGAGGAGGAGGAGGAAGA 47
                                                                                                                                                                                                                                                                                                                                                                                                 Bayer pharmaceuticals Corporation
Eveleigh, Deepa
Bigwood, Douglas
                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pharmaceuticals Corporation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               73.3%;
87.2%;
                                                                                                                                                                Score 37.4; DB 6; Length 3994;
Pred. No. 0.028;
0; Mismatches 6; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 37.4; DB 1
Pred. No. 0.028;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0,
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CURRENT APPLICATION NUMBER: US/10/417,375A
CURRENT FILING DATE: 2003-04-15
NUMBER OF SEQ ID NOS: 176
SEQ ID NO 167
SEQ ID NO 167
LENGTH: 150085

TYPE: DNA
ORGANISM: Mus musculus

US-10-417-375A-167/c

Sequence 167, Application US/10417375A GENERAL INFORMATION:

APPLICANT: David W. Morris
APPLICANT: Marc Malandro
TITLE OF INVENTION: Movel Therapeutic Targets in Cancer
FILE REFERENCE: 529452001600

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2 AGGATGAAGCTGAAGAGGAGGAGGAAGAAGAGGAGGAGGAAGAAGAG 48

Matches

Local

Similarity

76.5%; 89.4%;

Conservative

Score 39; DB 6; Pred. No. 0.013; 0; Mismatches 5

Length 54303; Indels

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Gaps

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0,

0

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RESULT 8
PCT-US03-32805-1
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; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-642-946-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 1, Application PC/TUS0332805 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 73.3%;
Best Local Similarity 87.2%;
Matches 41; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQ ID NO :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TITLE OF INVENTION: Infarction
FILE REFERENCE: 2345.2048002
CURRENT APPLICATION NUMBER: PCT/US03/32805
CURRENT FILING DATE: 2003-10-16
PRIOR APPLICATION NUMBER: 60/419,432
PRIOR FILING DATE: 2002-10-17
NUMBER OF SEQ ID NOS: 535
SOFTMARE: FABLSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQ ID NO 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CURRENT FILING DATE: 2003-08-18
PRIOR APPLICATION NUMBER: US/09/957,956
PRIOR FILING DATE: 2001-09-21
PRIOR APPLICATION NUMBER: US 60/234,422
PRIOR FILING DATE: 2001-09-21
NUMBER OF SEQ ID NOS: 8
SOFTWARE: Patentin version 3.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: deCODE genetics ehf.
APPLICANT: Helgadottir, Anna
APPLICANT: Gulcher, Jeffrey R.
APPLICANT: Manolescu, Andrei
TITLE OF INVENTION: Susceptibility Gene for Myocardial
TITLE OF INVENTION: Infarction
NAME/KEY: misc_feature
                                       NAME/KEY: misc_feature
LOCATION: (300892)...(300991)
OTHER_INFORMATION: n = A,T,C or G
                                                                                                                   NAME/KEY: misc feature
LOCATION: (279545)...(279644)
OTHER INFORMATION: n = A,T,C
                                                                                                                                                                                                  NAME/KEY: misc_feature
LOCATION: (272544)...(272643)
OTHER INFORMATION: n = A,T,C
                                                                                                                                                                                                                                                                              NAME/KEY: misc_feature
LOCATION: (269991)...(270091)
OTHER INFORMATION: n = A,T,C
                                                                                                                                                                                                                                                                                                                                                           NAME/KEY: misc_festure
LOCATION: 248521
OTHER INFORMATION: n = A,T,C or
                                                                                                                                                                                                                                                                                                                                                                                                                                        FEATURE:
NAME/KEY: misc_feature
LOCATION: (154988)...(155087)
OTHER INFORMATION: n = A,T,C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FEATURE:
NAME/KEY: misc_feature
LOCATION: (70677)...(70776)
OTHER INFORMATION: n = A,T,C or G
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                                                                                                                                                                                      FEATURE
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Pred. No. 0.033;
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                                                                                                    US-10-417-375A-1
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                                                Query Match 72.9%;
Best Local Similarity 84.0%;
Matches 42; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
                                                                                                         ORGANISM: Mus musculus
FEATURE:
NAME/KEY: misc_feature
LOCATION: (1)...(310122)
OTHER INFORMATION: n = A,T,C or G
                                                                                                                                                                            TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME/KEY: misc_feature
LOCATION: (396625)...(396724)
OTHER INFORMATION: n = A,T, C
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LOCATION: (391524)...(391623)
OTHER_INFORMATION: n = A,T,C or G
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LOCATION: (350504)...(350603)
OTHER INFORMATION: n = A,T,C
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NAME/KEY: misc_feature
LOCATION: (345190)...(345289)
OTHER INFORMATION: n = A,T,C
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LOCATION: (341698)...(341698)
OTHER INFORMATION: n = A,T,C
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NAME/KEY: misc_feature
LOCATION: (332849)...(332948)
OTHER_INFORMATION: n = A,T,C or
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OTHER INFORMATION: n = A,T,C
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51856 GAGGAGGAAGATGAAGATGAAGATGAGGAGGAGGAAGA
               1 GAGGATGAAGCTGAAGAGGAGGAGGAAGAGGAGGAGGAAGA 47
                                                                                                                                                                                         310122
                                                                                                                                                                                                                                                                                                                                                                                                                                                  41; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                              73.3%;
87.2%;
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                                                  0; Mismatches
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                                                              Score 37.2; DB 6; Pred. No. 0.042;
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Pred. No. 0.038;
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                                                                        Length 310122;
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RESULT 10 US-10-767-701-24209

Sequence 24209, Application US/10767701 GENERAL INFORMATION:

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INFORMATION: US/10767471

APPLICANT: CARGILL, Michele et al.

TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH

TITLE OF INVENTION: RHEUMATOID ARTHRITIS, METHODS OF DETECTION AND USES THEREOF

TITLE REFERENCE: CLOOLSOE

CURRENT APPLICATION NUMBER: US/10/767,471

FILE REFERENCE: CD01505

CURRENT PILING DATE: 5031

CURRENT FILING DATE: 3031

CURRENT FILING DATE: 
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FEATURE: SORGHATION: Clone ID: 30932345
OTHER INFORMATION: Clone ID: 30972345
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local S
Matches 41
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ORGANISM: Homo sapiens

FATURE: misc_feature

NAME/KEY: misc_feature

ORGANION: (1) -- (34304)

I LOCATION: (1) -- (34304)

OTHER INFORMATION: n = A,T,C or G, or insertion/deletion polymorphism (see Tables 1 or Corner in the corne
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Best Local S
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US-10-417-375A-79
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atch similarity 85.4%;
cal Similarity conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: DNA MUB MUBCULUB ORGANISM MUB MUBCULUB US-10-417-375A-79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          9950 GANGANGANGANGGAGGAGGAGGAGGANGGTGGANGAG 9997
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41; Conserva
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milarity 85.4%; 0
Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 36.8; DB 6; Length 34304; pred, No. 0.046; _________.
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Sequence 63, Application US/10417375A
Sequence 63, Application US/10417375A
Sequence 63, Application US/10417375A
SEREAL INFORMATION: Morris
SEPLICANT: Marc Malandro
APPLICANT: Marc Malandro
APPLICANT: Marc Movel Therapeutic Targets in Cancer
FILE RESENCE: 522452001600 US/10/417,375A
FILE RESENCE: 522452001600 US/10/417,375A
FILE RESENCE: 522452001600
CURRENT APPLICATION NUMBER: 2003-04-15
CURRENT FILING DATE: 2003-04-15
SUMBER OF SEQ ID NOS: 176
SUMBER OF FASTSEQ for Windows Version 4.0
SOFTWARE: 319715
LENGTH: 219715
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Best Local S:
Best Local 41.
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US-10-417-375A-63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-10-767-701-26619/C
Sequence 26619, Application US/10767701
Sequence 26619, Application Sequence 26619, Application Sequence 26619, Application Sequence 26619, Application Septication 
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NAME/KEY: misc_feature
NAME/KEY: misc_feature
NAME/KEY: misc_feature
NAME/KEY: misc_feature
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Best Local S
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ch inilarity 85.4%;
11 Similarity 85.4%;
41; Conservative
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US-10-767-701-26619
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Matches
                                                                                                                                                                                                                                                                                RESULT 15
US-10-767-701-15708/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
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ch milarity 85.1%; I
l Similarity 0;
40; Conservative
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Pred: No. 0.047; 7; Indels 0;
Mismatches
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Pred. No. 0.052; 7;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         score 35.8; DB 6; pred. No. 0.063; 7; pred. No. 0.063; 7; 0; Mismatches
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Sequence 15708, Application US/10767701

GENERAL INFORMATION:
APPLICANT: Kovalic, David K.
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof For Plant Improvement
FILE REFERENCE: 38-21(53535)
ICURENT FILING DATE: 2004-01-29
INVESTE OF SEQ ID NOS: 63128
SEQ ID NO 15708
SEQ ID NO 15708
SEQ ID NO 15708
SEQ ID NOS: 63128
SEQ ID NOS
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No.
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Maximum
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Database
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Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Title:
Perfect score:
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                                                                                                       Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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                                                     Score
  51
42
41.6
41.6
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  100.0
82.4
81.6
81.6
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Match Length DB
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11:
12:
13:
14:
15:
16:
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Gapop 10.0 , Gapext 1.0
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Copyright (c) 1993 - 2004 Compugen Ltd.
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AY416856 Homo sapi
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ACCESSION VERSION KEYWORDS SOURCE ORGANISM TITLE 1 (bases 1 to 1353)
Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A.,
Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,
Adams,M.D. and Cargill,M.
Inferring nonneutral evolution from human-chimp-mouse orthologous Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejariwal, A.,
Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B.,
Ferriera, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J.,
Adams, M.D. and Cargill, M. gene trios Science 302 (5652), 1960-1963 (2003) 14671302 Homo sapiens Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. AY416856 13:
Homo sapiens HCM6030 gene,
genomic survey sequence.
AY416856 Direct Submission Homo sapiens (human) AY416856.1 GI:39772816 1353 bp DNA linear GSS 12-DEC-2 1e, VIRTUAL TRANSCRIPT, partial sequence, GSS 12-DEC-2003

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ECAA2BAR
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Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
1 (bases 1 to 430)
                                                                                                   RPCI-23-63A7.TJ RPCI-23 Mus musculus
                                                                                                                                                                                                                       l Similarity
45; Conserva
                                     Mus musculus
                                            Mus musculus (house mouse)
                                                                                    genomic survey sequence AZ223727
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           880
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                                                                                                                       AZ223727
                                                                                                                                                                                        Submitted (14-SEP-2001) MRC Human Ge Centre Hinxton, Cambridge, CB10 1SB.
                                                                                                                                                                                                                                                                                                                                       biohelp@hgmp.mrc.ac.uk
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Equus caballus (horse)
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GSS; Alpha2 adrenergic
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This sequence was made by sequencing genomic exons and ordering them based on alignment.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Similarity
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adrenergic receptor gene
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                                                                                                                                                                                                                                                                              /organism="Equus caballus"
/mol_type="genomic DNA"
/db_xref="taxon:9796"
                                                                                                                                                                                                                                                                                                                             ocation/Qualifiers
                                                                       GI:8531776
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|mol_type="genomic DNA"
|db_xref="taxon:9606"
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90.0%;
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Pred. No. 39;
0; Mismatches
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Perissodactyla; Equidae; Equus.
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Pred. No. 0.7
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    Craniata; Vertebrata; Euteleostomi;
Sciurognathi; Muridae; Murinae; Mus
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SB. UK Email:
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RPCI-23-63A7,
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subtype b,
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                                                                                                                                                                                                                                                                               103
                                                                                                    Rattus
                                                                                                                                                                                                                                                                                                                           44;
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Unpublished (1998)
Contact: Lee, NH
The Institute for Genomic Research
9712, Medical Center Drive, Rockvil
                                                                                                        Lee, N.H., Glodek, A., Chandra, I., Mason, T.M., Kerlavage, A.R. and Adams, M.D.
Rat Genome Project: Generation of a Rat EST
                                                                                                                                                                                                                                                                                  EST.
Rattus sp.
                                                                                                                                                                                                                                                                                                                                             AA943361
EST198860 Normalized
RBRAI64 3' end, mRNA
AA943361
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Mammalia; Eutheria;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Email: szhao@tigr.org
Clones are derived from the mouse BAC library RPCI-23. For BAC
Clones are derived from the mouse BAC library RPCI-23. For BAC
Clones are derived from the mouse BAC library availability, please contact Pieter de Jong
(pieter@dejong.med.buffalo.edu). Clones may be purchased from
BACPAC Resources (http://bacpac.med.buffalo.edu/orderingframe.htm)
or from Resea ch Genetics (info@resgen.com). BAC end page:
http://www.tigr.org/tdb/bac_ends/mouse/bac_end_intro.html
Seq primer: Sp6
Class: BAC ends.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Contact: Shaying Zhao
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Tel: 301 838 0200
Fax: 301 838 0208
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Unpublished (1999)
Other_GSSs: RPCI-23-63A7.TV
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Mouse BAC End Sequences from Library RPCI-23
(301) -838-3529
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /Clone lib="RPCI-23"
//note=Torgan: Kidney/Brain; Vector: pBACe3.6; Site 1:
ECORI; Site 2: ECORI; Female C57BL/6J mouse kidney and/or
brain genomic DNA was isolated and partially digested
with a combination of ECORI and ECORI methylase. Size
Belected DNA was cloned into the pBACe3.6 vector at the
ECORI sites. The ligation products were transformed into
DH10B electrocompetent cells (BRL Life Technologies). "
                                                                                                                                                                                                                                                                                                                                                     469 bp
Normalized rat brain,
end, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /db_xref="taxon:10090"
/clone="RPCI-23-63A7"
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/strain="C57BL/6J"
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91.7%;
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Pred. No. 43;
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          Rockville,
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es Rattus
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                                                                                                                                             Quackenbush, J.,
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Best Local Similarity
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                                                                                                                                                                 source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     44;
                                                                                                                                                                                                                                                       The sequence contained an oligo-dT track that was present in the oligonucleotide that was used to prime the synthesis of first strand cDNA and therefore this may represent a bonafide poly A tail. The sequence tag present in the cDNA between the NotI site and the oligo-dT track served to identify it as a clone from the normalized corpus-striatum library cDNA Library Preparation: M.B. Soares Lab Clone distribution: clones will be available through Research Genetics (www.resgen.com) The following repetitive elements were found in this cDNA sequence: 365-436,
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Coordinated Laboratory for Computational Genomics University of Iowa 375 Newton Road, 4156 MEBRF, Iowa City, IA 52242, Tel: 319 335 8250 Fax: 319 335 9565
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Rattus norvegicus
Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BE097734 517 bp mRNA UI-R-BO1-aqb-a-11-0-UI.sl UI-R-BO1 Rattus UI-R-BO1-aqb-a-11-0-UI 3', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 GAGGATGAAGCTGAAGAGGAGGAGGAGGAGGAGGAGGAAGAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Fax: (301)-838-0208
Email: nhlee@tiar o
                                                                                                                                                                                                Seq primer: M13 Forward POLYA=Yes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Genome Res. 6 (9),
97044477
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 (bases 1 to 517)
Bonaldo, M.F., Lenno
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BE097734
                                                                                                                                                                                                                                             > (GGA) n#Simple
                                                                                                                                                                                                                                                                                                                                                                                                                                         Email: bento-soares@uiowa.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           discovery
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Rattus norvegicus (Norway rat)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             il: nhlee@tigr.org
primer: M13-21.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
/organism="Rattus norvegicus"
/mol_type="mRNA"
/strain="Sprague-Dawley"
/db_xref="taxon:10116"
/clone="UI-R-BO1-aqb-a-11-0-UI"
/dev_stage="adult"
/lab_host="BH10B (Life Technologies)"
/clone_lib="UI-R-BO1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /clone_lib="Normalized rat brain, Bento Soares"
/note="Organ: brain; Vector: pT7T3Pac; Site_1: EcoRI;
Site_2: Not1"
                                                                                                                                                                               ocation/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /db_xref="ATCC (inhost):2012877"
/db_xref="taxon:10118"
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91.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Lennon, G. and Soares, M.B.
                                                                                                                                                                                                                                           repeat
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Pred. No. 43
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CDNA clone
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VERSION
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CF795982/c
LOCUS
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Matches 44
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Best Local
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                                                                                                  Local Similarity
152
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                                                                             44;
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                                                                                                                                                                                                                                                                                                                                                                                                cross match v0.990329.
Plate: TMW8018 row: D
Seq primer: TAGAAGGCAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 (bases 1 to 552)
Smith, T.P.L., Freking, B.A., Ford, J.J., Vallet, J.L., Wise, T.A.,
Nonneman, D.J., Wray, J.E. and Keele, J.W.
Porcine EST collection using a normalized library constructed from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         892192\ MARC\ 4PIG\ Sus\ scrofa\ cDNA\ 3',\ mRNA\ sequence. CF795982
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 GAGGATGAAGCTGAAGAGGAGGAGGAGGAGGAGGAGGAGGAAGAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Single pass sequencing. Bases called with phred v0.020425.c and trimmed with the aid of the trim_alt option. Vector identified of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        USDA, ARS, US Meat Animal Research Center
PO Box 166, Clay Center, NE 68933-0166, USA
Tel: 402 762 4366
Fax: 402 762 4390
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           embryos representing early developmental stages Unpublished (2003)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sus scrofa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sus scrota (pig)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EST.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Email: smith@email.marc.usda.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Contact: Smith TPL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Similarity
GAGGATGAAGATGAAGAGGAGGACGAGGACGAGGAGGATGAAGAG
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                                                                             Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note="Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; The library (UI-R-BO1) is a Subtracted library derived from a mixtu of the following tissues: thalamus, cerebellum, hypothalamus, medulla, pons, midbrain, cerebral cortex, corpus striatum and hippocampus. For a detailed description of the library from which this clone was
                                                                                                                                                                      /clone lib="MARC 4PIG"
/note="Vector: pcDNA3.1; Site 1: EcoRI; Site 2: NotI;
Library made with combined RNA from day-10, day-13,
day-15, day-25, and day-30 whole embryos."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TAG_TISSUE=corpus-striatum
TAG_LIB=UI-R-BO1
TAG_SEQ=CTAGG"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              derived, please visit our web site at ratest.eng.uiowa.edu. The subtraction has been previously described in (Bonaldo, Lennon and Soares, Genome Research
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 6:791-806, 1996)
                                                                                                                                                                                                                                                                                                  organism="Sus scrofa"
/mol_type="mRNA"
/db_xref="taxon:9823"
                                                                                                                                                                                                                                                                                                                                                                               Location/Qualifiers
                                                                                                                                                                                                                                                          tissue_type="pooled"
lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                 . 552
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                                                                                              81.6%;
91.7%;
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91.7%;
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                                                                                              Score 41.6; DB Pred. No. 44;
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105
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RESULT 7
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AUTHORS
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AZ288043/c
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Best Local
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                                                                                                                                                                                                                                                                             JOURNAL
                                                                                                                                                                                                                                                                                                TITLE
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AJ517718 Dreissena polymorpha
chron35, mRNA sequence.
AJ517718
AJ517718 GI:25778429
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Dreissena polymorpha
Eukaryota; Metazoa; Mollusca; Bivalvia; Heteroconchia; Veneroida;
Dreissenoidea; Dreissenidae; Dreissena.
1 (bases 1 to 604)
Bultelle,F., Panchout,M., Leboulenger,F. and Danger,J.-M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Contact: Danger J-M
Contact: Danger J-M
Laboratory of Ecotoxicology
University of Le Havre
25 rue P. Lebon, 76058 Le Havre CEDEX,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RPCI-23-102K10.TV RPCI-23 Mus musculus RPCI-23-102K10, genomic survey and AZZBARAY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Dreissena polymorpha
Unpublished (2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Effect of xenobiotics on the transcriptome of the zebra mussel
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                                                                                                                                                                                                                                                                                                Akinret,B., Levins,M., Mcgann,S., Tsegaye,G., Jong,P. and Fraser,C.M.
Mouse BAC End Sequences from Library RPCI-23
                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 713)
or from Resea ch Genetics () http://www.tigr.org/tdb/bac_
  Clones are derived from the mouse BAC library RPCI-23. For BAC Clones are derived from the mouse BAC library availability, please contact Pieter de Jong Library availability, cedu . Clones may be purchased from Epiceres (http://bacpac.med.buffalo.edu/orderingframe.htm) BAC Resources (http://www.tigr.org/tdb/bac_ends/mouse/bac_end_intro.html
                                                                                                                                                                           Contact: Shaying Zhao
Department of Eukaryotic Genomics
Department for Genomic Research
The Institute for Genomic Research
9712 Medical Center Dr., Rockville,
                                                                                                                                                                                                                                                             Unpublished (1999)
Other_GSSs: RPCI-23-102K10.TJ
                                                                                                                                                                                                                                                                                                                                                       Zhao, S., Nierman, W., Feldblyum, T.,
                                                                                                                                                                                                                                                                                                                                                                                                                                        Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AZ288043
AZ288043.1 GI:9529829
                                                                                                                                     Tel: 301 838 0200
Fax: 301 838 0208
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mus musculus (house mouse)
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                                                                                                                       3mail: szhao@tigr.org
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/clone_lib="Drei
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     organism="Dreissena polymorpha"/mol_type="mRNA"
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91.7%;
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Pred. No. 4
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Dreissena polymorpha cDNA clone
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                                                                                                                                                                                                                                                                                                                                                               Malek, J., Shatsman, S.,
                                                                                                                                                                                 MD 20850, USA
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RESULT 9
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Query Match
Best Local Similarity
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Class: BAC ends.
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BI067787

BI067787

BI067787

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BI0677.124 normalized chicken fat cDNA library Gallus gallus cDNA clone pgfln.pk007.124 5' similar to gi|4506411

ref|NP 002874.1| Ran GTPase activating protein 1; Fugl [Homo sapiens] gi|1418178 ref|XP 010014.1| Ran GTPase activating protein 1 [Homo sapiens] sp|P46060|RGP1-HUMAN RAN-GTPASE ACTIVATING PROTEIN 1 pir 138146 RanGAP1 - human pir |JC, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Plate: 102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                44;
                                                                                                                                                                                                                                                                                                                                                                                                           Cogburn, L.A., Morgan, R.W. and Burnside, J. Chicken ESTs from fat Unpublished (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gallus gallus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Eukaryota; Metazoa; Chordata; Galliformes; Phasianidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              BI067787.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Archosauria; Aves; Neognathae; Phasianinae; Gallus.
1 (bases 1 to 640)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gallus gallus (chicken)
                                                                                                                                                                                                                                                                                                                                     Tel: 302-831-1335
                                                                                                                                                                                                                                                                                                                                                       University of Delaware Townsend Hall, Newark,
                                                                                                                                                                                                                                                                                                                                                                                            Contact: Larry A. Cogburn
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Similarity
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                                                                                                                                                                                                                                                                                                                  302-831-2822
                                                                                                                                                                                                                                                                                              cogburn@udel.edu,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /clone lib="RPCI-23"
/note="Togran: Kidney/Brain; Vector: pBACe3.6; Site 1:
/note="Togran: Kidney/Brain; Vector: pBACe3.6; Site 1:
RECORI; Site 2: EcoRI; Female C57BL/6J mouse kidney and/or
Brain genomIc DNA was isolated and partially digested
with a combination of EcoRI and EcoRI Methylase. Size
selected DNA was cloned into the pBACe3.6 vector at the
ECORI sites. The ligation products were transformed into
DH10B electrocompetent cells (BRL hife Technologies). "
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/strain="C57BL/6J"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           gex="Female"
                                                                                                                                                      /clone="pgf1n.pk007.124"
/sex="Male and Female"
                                                                                                                                                                                                           /organism="Gallus gallus"
/mol type="mRNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       lab_host="DH10B"
                                                                        /lab host="E.coli EMDH10B"
/clone_lib="normalized chicken
/note="Vector: pSPORT1"
                                                                                                                                                                                                 /db xref="taxon:9031"
                                                                                                                                                                                                                                                                         ocation/Qualifiers
                                                                                                                                       tissue_type="fat"
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91.7%;
  79.6%;
91.5%;
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Pred. No. 46;
    Score 40.6;
Pred. No. 71;
                                                                                                                                                                                                                                                                                                  www.chickest.udel.edu.
                                                                                                                                                                                                                                                                                                                                                              USA
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BU121352
BU121352
BU121352.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Clones are derived from the rat BAC library CHORI-230 (http://www.chori.org/bacpac/rat230.htm). For BAC library availability, please contact Fieter de Jong (pdejong@mail.cho.org). Clones may be purchased from BACPAC Resources (http://www.chori.org/bacpac/or ering_information.htm). BAC end page: http://www.tigr.org/tdb/bac_ends/rat/bac_end_intro.html plate: 4 row: L column: 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Contact: Shaying Zhao Department of Eukaryotic Genomics The Institute for Genomic Research 9712 Medical Center Dr., Rockville, Tel: 301 838 0200 Fax: 301 838 0208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Riggs, F., de Jong, P. a
Rat BAC End Sequences
Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; I
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              BH309086 668 bp DNA CH230-4L16.TV CHORI-230 Segment 1 Rattus CH230-4L16, genomic survey sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Rattus norvegicus (Norway rat)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Email: szhao@tigr.org
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                                                                                                                                                                                                                                                                                                                                      /cell_type="Brain"
/clone_lib="CHORI-230 Segment 1"
/note="Vector: pTARBAC2.1; Site 1: EcoRI;
CHORI-230 Rat (BN/S8NH8d/MCW) BĀC library
                                                                                                                                                                                                                                                                                                                                                                                                                           /organism="Rattus norvegicus"
/mol type="genomic DNA"
/strain="BN/SsNHsd/MCW"
/db xref="taxon:10116"
/clone="CH230-4L16"
                                                                                                                                                                                                                                                                                                                         Pieter de Jong"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ocation/Qualifiers
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 GI:25331126
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91.5%;
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Pred. No. 71;
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s cDNA clone ChEST145o16 5', mRNA
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Russell, D.,
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22335534
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; E
Mammalla; Eutheria; Primates; Catarrhini; Hominidae;
1 (bases 1 to 753)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collect
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                    43;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EST.

Gallus gallus (chicken)

Gallus gallus
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601504406F1 NIH_MGC_71 Homo
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Phasianinae; Gallus.
1 (bases 1 to 723)
1 (bases 1 to 723)
Boardman, P.E., Sanz-Ezquerro, J., Overton, I.M., E
Fong, W.T., Tickle, C., Brown, W.R.A., Wilson, S.A.
A Comprehensive Collection of Chicken cDNAs
Curr. Biol. 12 (22), 1965-1969 (2002)
                                                                                                                                                             Homo sapiens
                                                                                                                                                                                                  EST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Contact: Simon Hubbard
Department of Biomolecular Sciences
University of Manchester Institute of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
                                                                                                                                                                            Homo sapiens (human)
                                                                                                                                                                                                                 BE613618.1
                                                                                                                                                                                                                                    BE613618
                                                                                                                                                                                                                                                 mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Tel: 01612008930
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Similarity
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                                                                                                                                                                                                                                                                                                                                                                             GAGGATGAAGCTGAAGAGGAGGAAGAAGAGGAGGAGGAAGA 47
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Box 88, Manchester,
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Simon.Hubbard@umist.ac.uk.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note=Worgan: kidney + adrenal; Vector: pBluescript II KS(+); Site 1: EcoRI; Site 2: Not1; Modification of pBluescript II KS(+) [Stratagene] vector to accommodate cDNA produced with the T-trimmed protocol (Construction of uni-directionally cloned cDNA libraries from messenger RNA for improved 3' end DNA sequencing by Glenn Fu, et al. U.S. Patent # 6, 387,624). Cut pBluescript II KS(+) with NotI and EcoRI. Ligate in double stranded adaptor containing BsgI and BamHI sites
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /mol_type="mRNA"
/strain="Compton Line
/db_xref="taxon:9031"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     [5'ggccgcgtgcagccccggatccgaaaaaaag]
[5'aattcttttttcggatccgggctgcacgc] "
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /dev_stage="adult"
/lab_host="DH10B"
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                                                                                                                                                                                                                 GI:9895215
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91.5%;
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s cDNA
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                                                                        Collection (MGC)
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                                                                                                                                             Euteleostomi;
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Class: transposon-tagged
                                                                                                                                                                                                                                                           Email: anuj.kumar@yale.edu
te of mTn-3xHA/lacZ insertion.
Seg primer: GGCCTTCTTTCTTTGGAAGTAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ross-Macdonald, P., Roemer, T., Coelho, P.S.R., Agarwal, S., Kumar, A., desEtages, S.A., Cheung, K.-H., Sheehan, A., Symoniatis, D., Jansen, R., Umansky, L., Heidtman, M., Nelson, K., Iwasaki, H., Kanada, D., Lugo, R., Hager, K., Miller, P., Roeder, G.S. and Snyder, M., Kanada, D., Lugo, R., Large-Scale Analysis of the Yeast Genome by Transposon Tagging and
                                                                                                                                                                                                                                                                                                                                                                                     Contact: Kumar A
Michael Snyder, Dept.
Yale University
                                                                                                                                                                                                                                                                                                                                                                                                                                      Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes; Saccharomycetales; Saccharomycetaceae; Saccharomyces.

1 (bases 1 to 797)
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V130F6 mTn-3xHA/lacZ Insertion Library,
cerevisiae genomic 5', genomic survey s
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AQ875889
AQ875889.1 GI:6288133
GSS.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Box 208103, New Haven, CT 06520-8103, USA
203 432 9949
203 432 6161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
/Clone lib=mTn-3xHA/lacZ Insertion Library, strain Y2278
/note="Vector: pHSS6-Sal; A yeast genomic DNA library
without 2 micron or mitochondrial DNA was prepared in
pHSS6-Sal; genomic DNA was size-fractionated (DNA of
roughly 2-3 kb in length) prior to cloning. This library
                                                                                                                     /mol_type="genomic_DNA"
/strain="72278 - S288C background, cir(0) rho(0)"
/db_xref="taxon:4932"
                                                                                                                                                                /organism="Saccharomyces cerevisiae"
/mol_type="genomic DNA"
                                                                                                                                                                                                                               ocation/Qualifiers
                                                                                                                 lab_host="E. coli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /clone="IMAGE:3906193"
/tissue_type="leiomyosarcoma"
/lab_host="DH108 (phage-resistant)"
/clone_lib="NIH_MGC_71"
/note="Organ: uTerus; Vector: pCMV-SPORT6; Site_1: Not1;
Site_2: SalI; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 2.1 kb. "
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
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91.5%;
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Pred. No. 72;
0; Mismatches
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8 Saccharomyces
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KEYWORDS
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BZ227940/c
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REFERENCE AUTHORS

VERSION KEYWORDS

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SOURCE

ORGANISM

RESULT 13 AQ875889 LOCUS

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27

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Query Match Best Local ( Matches

43;

FEATURES

source

COMMENT

JOURNAL TITLE

FEATURES

source

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Email: stakeostigr.org

Email: stakeostigr.org

Clones are derived from the rat BAC library CHORI-230

(http://www.chori.org/bacpac/rat230.htm). For BAC library

availability, please contact Pieter de Jong (pdejong@mail.cho.org).

Clones may be purchased from BACPAC Resources

(http://www.chori.org/bacpac/or ering information.htm). BAC end

page: http://www.tigr.org/tdb/bac_ends/rat/bac_end_intro.html
                                                                                         Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Contact: Shaying Zhao
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  l (bases 1 to 826)
Zhao, S., Shetty, J., Shatsman, S., Tsegaye, G.,
Shvartsbeyn, A., Gebregeorgis, E., Overton, L.,
Riggs, F., de Jong, P. and Fraser, C.M.
Rat BAC End Sequences from Library CHORI-230
Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Rattus norvegi
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CH230-400D22, genomic survey sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        43;
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                                                                        Conservative
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301 838 0208
                                                                                                                                                       /clone lib="CHORI-230 Segment 2"
/note="Vector: PTARBAC1.3; Site 1: MboI; S
CHORI-230 Rat (BN/SBNH8d/MCW) BĀC library
                                                                                                                                                                                                               /cell_type="Brain"
                                                                                                                                                                                                                                                         /organism="Rattus norvegicus"
/mol_type="genomic DNA"
/strain="BN/S8NHsd/MCW"
/db_xref="taxon:10116"
                                                                                                                                                                                                                                                                                                                                       Location/Qualifiers
                                                                                                                                                                                                                                           clone="CH230-400D22"
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                                                                                    79.6%;
91.5%;
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91.5%;
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Pred. No. 73;
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Pred. No. 73;
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Rattus norvegicus genomic clone
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library produced by
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URA3, and tet resistance.
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Russell, D.,
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Search completed: March 2, 2004, 08:34:35 Job time: 2156 secs
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

E 1 (bases 1 to 873)

E NIH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

LUpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-remail.nih.gov

Tissue Procurement: ATCC/DCTD/DTP

cDNA Library Preparation: Life Technologies, Inc.

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Agencourt Bioscience Corporation

Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:

http://image.llnl.gov

Plate: LLAM13316 row: m column: 17

High quality sequence stop: 703.

1 1 272
                                                                                       873 bp mRNA linear EST 02-WAY-2002 AGENCOURT_7560029 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:6055864 5', mRNA sequence.
80231724 B0231724.1 GI:20413124 EST.
                                                                                                                      1 GAGGATGAAGCTGAAGAGGAGGAAGAAGAGGAGGAGGAGGAGGAAGA 47
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Homo sapiens
                                                                                                                                                                                                                                                                                       /tissue_type="melanotic melanoma"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH_MGC_72"
/note="Organ: skin; Vector: pCMV-SPORT6; Site_1: Not1;
Site_2: SalI; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 2 kb. Library constructed by Life
Technologies."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     /organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:6055864"
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Copyright (c) 1993 - 2004 Compugen Ltd.
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is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

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Wang, S.Y. and Pilkey, D.T.
Identification in islets
2-adrenergic receptor
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Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
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Langerhans, mRNA Partial, 828 nt].
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Diabetes 43 (1), 127-136 (1994)
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y (NCBI gibbsg 140730) from the original journal article. 
sequence comes from Fig. 1. 
Location/Qualifiers
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                                                                                 /translation="CTSSIVHLCAISLDRYWAVSRALEYNSKRTPRRIKCIILTVWLIAVISLPPLIYKGDQGPQPRGRPQCKLMQBAWYILASSIGSFFAPCLIMILVYLRIYLIAKRSNRRGPRAKGGPQGESKQPRPDHGGALASAKLPALASVASAREVNGHSKSTGE KEEGETPEDTGTRALPASWAALPNSGQGQKEGVCGGSPEDEAEEEEEEEEEDQAVP VSPASACSPPLQQPQGSRVLATLRGQVLLGRGVGAIGGQWWRRRAQLTREKRFTFVLA
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/product="alpha 2-adrenergic receptor"
/protein_id="AAP14006_1"
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/mol_type="mRNA"
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order(S67317.1:1. .130,1. ...
/gene="alpha.2-adrenergic r/
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                                                                                                                           Small, K.M., Brown, K.M., Forbes, S.L. and Lig
Direct Submission
Submitted (26-OCT-2000) Internal Medicine,
Cincinnati, 231 Bethesda Ave, Cincinnati, (
Location/Qualifiers
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                                                                                                                                                                                                                              Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleos Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 1344)
Small, K.M., Brown, K.M., Forbes, S.L. and Liggett, S.B. Polymorphic deletion of three intracellular acidic residues alpha 2B-adrenergic receptor decreases G protein-coupled reckinase-mediated phosphorylation and desensitization
J. Biol. Chem. 276 (7), 4917-4922 (2001)
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Alpha-2 adrenergic receptor polymorphisms
Patent: WO 0179561-A 2 25-OCT-2001;
Liggett, Stephen B. (US); Small, Kersten
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/db_xref="taxon:9606"
/chromosome="2"
<1...1344
                   <1. .>1344
/gene="ADRA2B"
       'product="alpha
                                                                                             /organism="Homo sapiens"
/mol_type="genomic DNA"
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/mol_type="unassigned DN/
/db_xref="taxon:9606"
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Pred. No. 7e-05;
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5 (bases 1 to 22842)

Waterston,R.H.

Direct Submission
Submitted (23-OCT-2001) Genome Sequencing Center, Washington University School of Medicine, 4444 Forest Park Parkway, St.

MO 63108, USA
6 (bases 1 to 22842)
                                                                                                                                                                                                                4 (bases 1 to 22842)
Waterston,R.H.
Direct Submission
Submitted (20-OCT-2001) Genome Sequencing Center, Washington University School of Medicine, 4444 Forest Park Parkway, St.
MO 63108, USA
5 (bases 1 to 22842)
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Unpublished (10.2002)
3 (bases 1 to 22042)
Waterston, R.H.
Direct Submission
Submitted (19-JUL-2001) Genome Sequencing Center, Washington Submitted (20-JUL-2001) Genome Sequencing Center (20-JUL-2001) Genome Sequencing 
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Homo Bapiens BAC clone RP11-139J6
AC092603 AC073396
AC092603.2 GI:16303539
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Martinka,S., Abbott,A., Hawkins,M., Elliott,G. and Doebber,A. The sequence of Homo sapiens BAC clone RP11-139J6 Unpublished (2001)
3 (bases 1 to 22842)
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Sulston, J.E. and Waterston, R.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Toward a complete human genome sequence Genome Res. 8 (11), 1097-1108 (1998)
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APQNLFLVSLAAADILVATLIIPSLARIKAYYFRRTWCEVYLALDVLFCTSSIVH
LCAISLDRYMAVSRALEVSNSKTPRRTIKCIILTVWLIAAVISLPPLIYKDQGPQFRG
RPQCKLNQEAWYILASSIGSFFAPCLIMILVYLRIYLLAKRSWRRGPRAKGGPCQGES
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LPNSGQGKEGVCGASPEDEAEEEEEEEEECEPQAPPVSPAAACSPPLQQPQGSRVLA
TLRGQVLLGRGYGAIGGGWMRRRAQLTMEKRFTFVLAVVIGVEVLCWFPFFFSYSLGA
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TLRGCYCHGLFQFFFWIGYCNSSLNPVIYTIFNQDFRRAFRRILCRPWTQTAW"
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Accession Number AF005900; polymorphic sequence lacks
three glu residues at this location"
/frequency="Caucasians 0.31; African-Americans 0.12"
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/db_xref="GI:12698670"
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. 7e-05;
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Submitted (01-MAR-2002) Department of Genetics, Washington
University, 4444 Forest Park Avenue, St. Louis, Missouri 63
On Oct 20, 2001 this sequence version replaced gi:14916188.
                                                                                                                                                                                                                                                                                                           Waterston, R.
                                                                       Center: Washington University Genome Sequencing Center code: WUGSC
Web site: http://genome.wustl.edu/gsc
Contact: sapiens@watson.wustl.edu
                                                                                                                                                                              .---- Genome Center
Drafting Center: WIBR
                     Center project name: H_NH0139J06
                                                  Summary Statistics
                                                                                                                                                                                                                                   63108, USA
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NOTICE: This sequence may not represent the entire insert of this clone. It may be shorter because we only sequence overlapping clone sections once, or longer because we provide a small overlap between neighboring data submissions.

all regions were double stranded, sequenced with an alternate chemistry, or covered by high quality data (i.e., bhred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by sequence from more than one subclone; and the assembly was confirmed by MAPPING INFORMATION: This sequence was finished as follows unless otherwise noted: restriction digest.

Mapping information for this clone was provided by Dr. John D. McPherson, Department of Genetics, Washington University, St. 1 MO. For additional information about the map position of this sequence, see http://genome.wustl.edu/gsc Louis

The RPCI-11 human BAC library was made from the blood of one male donor, as described by Osoegawa, K., Woon, P.Y., Zhao, B., Frengen, E. Tateno, M., Catanese, J.J. and de Jong, P.J. (1998) An improved approach for construction of bacterial artificial chromosome libraries. Genomics 51:1-8. The clone may be obtained either from Research Genetics, Inc. (http://www.resgen.com) or Pieter de Jong and coworkers at http://www.chori.org SOURCE INFORMATION: pBACe3.6 Frengen, E.,

NEIGHBORING SEQUENCE INFORMATION:
The clone sequenced to the left is RP11-401C13, 2000 bp overlap;
the clone sequenced to the right is RP11-574O17, 2000 bp overlap.
Actual end of this clone is at base position 48999 of RP11-574O17.

Polymorphisms have been identified between AC013272 and AC092603

The sequence of AC073396 has been incorporated into AC092603 Location/Qualifiers clone="RP11-139J6" map="2 'chromosome="2" /mol\_type="genomic Da /db\_xref="taxon:9606" organism="Homo sapiens .22842

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FEATURES
repeat_region
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1495. .1665
  /rpt_family="Alu"
2812. .2918
                                                                          /rpt_family="(TG)n"
1424. .1449
                                                                                                   /rpt_family="MIR"
1377. .1424
                                                                                                                                      clone_lib="RPCI-11"
                                     _family="Alu"
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20027. 20027
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15110. 15648
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                                                                                                                                                                                                                                                                      / Ypt family="(TCC)n"
14762. 14822
/note="similar to Homo sapiens EST AL544609
(NID:912877089)"
                                                                                                                                                                                                       note="CpG_island (%GC=74.2, o/e=0.90, #CpGs=191)"
[4900. .15218
'note="similar to Homo sapiens EST AL544609
[NID:g12877089)"
                                                                                                                                                                                                                                                              4849. .16413
                                                                                                                                                                                                                                                                                                                                                                             14060. .14247

note="similar to Homo

(NID:g12886265)"
                                                                                                                                                                                                                                                                                                                                        note="similar to Homo sapiens (NID:g12933576)"
                                                                                                                                                                                                                                                                                                                                                                                                                   /note="similar to Homo sapiens EST T39448 (NID:g647179)
                                                                                                                                                                                                                                                                                                                                                                                                                                        note="match to EST BF475329 (NID:g11546156)"
.4030. .14244
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               note="match to EST BF475329
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5541. .5566
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          note="match to EST AA887330 (NID:g3002438) oj40h05.sl"
2378. .12902
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                                  family="MER1_type"
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                                                                                                                                                                                               . .15487
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                                                                                                                                                                       scrofa EST AW785035 (NID:97841811)"
                                                                                                                                                                                                                                                                                                                                                                                    sapiens EST AL549866
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (NID:g11546156) "
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Direct Submission
Submitted (18-NOV-1999) M
University of Nijmegen, F
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        aar2B gene; alpha adrenergic receptor 2B. Phoca vitulina (harbor seal)
Phoca vitulina
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21082081
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Mammalia; Eutheria; Carnivora; Pinnipedia; Phocidae; Phoca
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 GAGGATGAAGCTGAAGAGGAGGAGGAGGAGGAGGAAGAGTGTGAACCCCAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Phoca vitulina partial aar2B
AJ251176
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51; Conserv
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                                                                                                                /COGON_Start=2
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/db_xref="GOA:Q9GL07"
/db_xref="GOA:Q9GL07"
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/PEERAEEEEEEEEEEEEEQALPASPASACSPPLPQPQGSRVLATLRGQYLLGRGVGTAS
GQWWRRRAQLTREKRPTFVLAVVIGVFVLCWFPFFFSYSLGAICPQHCKVPHGLF"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /organism="Phoca vitulina"
/mol_type="genomic DNA"
/db_xref="taxon:9720"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  gene="aar2B"
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1 1168
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22057. .22208
/note="match to EST AA836522 (NID:g2910841) od22d08.81"
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22057. .22471
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20537. .20973
                                  90.6%;
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Score 46.2; DB 4; Length 1168; Pred. No. 0.0017; 0; Mismatches 3; Indels 0
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Pred. No. 6.3e-05;
Mismatches 0;
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                                                                                                                                                                                                                                       46;
                                             Lama pacos partial adra2b gene i
AJ315941
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Lama pacos (alpaca)
Lama pacos
              AJ315941.1 GI:21212927
adra2b gene; alpha 2B adrenergic receptor.
                                                                                                                                                                                                     1 GAGGATGAAGCTGAAGAGGAGGAGGAGGAGGAGGAGGAGTGTGAACCCCCAG 51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Submitted (14-AUG-2002) Madsen O., 161 Biochemistry NWI, University of Nijmegen, PO.BOX 9101, 6500HB Nijmegen, NETHERLANDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Madsen,O., Willemsen,D., Ursing,B.M., Arnason,U. and de Jong,W.W. Molecular evolution of the mammalian alpha 2B adrenergic receptor Mol. Biol. Evol. 19 (12), 2150-2160 (2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Lama pacos partial adra2b adra2b-2 allele.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutelo
Mammalia; Eutheria; Cetartiodactyla; Tylopoda; Camelidae;
Lama pacos (alpaca)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Direct Submission
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Unpublished
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                                                                                                                                                                     GAGGAGGAGGCTGCAGAGGAGGAGGAGGAGGAGGAGAGTGTGAGCCTCAG 895
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                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                  /allele="adra2b-2"
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/protduct="alpha 2B adrenergic receptor"
/protdinct="alpha 2B adrenergic receptor"
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GKLPTLVSQLATAGEANGRPHPTGEKDEGETPEDPGTPALPNWPALPNSGQGQKEGV
CGTSPEEBAABEEEEEEECEPQALPASPASACSPPLQQPOVSRVLATLRGQVTLGRGV
CGTSPEEBAABEEEEEEECEPQALPASPASACSPPLQQPOVSRVLATLRGQVTLGRGV
                                                                                                                                                                                                                                                                                                                           GTSRGQWWRRRAQLTREKRETEVLAVVIGVEVLCWEPFFEFSYSLGAICPEHCKVPRGL
F"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                'gene="adra2b"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              'gene="adra2b"
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2b gene f
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                                                                 DNA linear MAM 22-MAY-2002 for alpha 2B adrenergic receptor.
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alpha 2B
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synthetic construct
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Mammalia; Eutheria;
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                                                                                      1. .6904
                                                                                                    ocation/Qualifiers
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/mol_type="genomic DNA"
/db_xref="taxon:30538"
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90.2%;
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Douady, C.J., Teeling, E., Ryder, O.A., Stanhope, M.J.,
and Springer, M.S.
                                                                                                                                                                                              Olek, A., Piepenbrock, C. and Berlin, K. Diagnosis of diseases associated with the Patent: WO 0200928-A 47 03-JAN-2002;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 GAGGATGAAGCTGAAGAGGAGGAGGAGGAGGAGGAGTGTGAACCCCAG
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CGTSPEEBAAEEEEAAEEEEEEEECEPQALPASPASACSPPLQQPQISRVLATLRGQV
LLGRCVGTSRGQWWRRRAQLTREKRFTFVLAVVIGVFVLCWFPFFFSYSLGAICPEHC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /product="alpha 2B adrenergic receptor"
/product="alpha 2B adrenergic receptor"
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/db_xref="GI:21212928"
/db_xref="GOA:QBMK51"
/db_xref="GOA:QBMK51"
/db_xref="SPTREMBL:QBMK51"
/db_xref="SPTREMBL:QBMK51"
/translation="AIAAVITFELLFTIFGNALVILAVLTSRSLRAPQNLFLVSLAPA
DILVATLIIPSGLANBELGYMYFRRYMCEVYLALDVLFCTSSIVHLCAISLDRYWAVS
RALEYNSKRTPRRIKCIILTVWLIAAVISLPPLIYKGDQSPQFRGRPQCKLNQEAWYI
LASSIGSFFRFCLIMILVYLAIYLIAKRSHRRGPRAKGGPGKGPGKDFGEVSAV
LASSIGSFFRFCLIMILVYLAIYLIAKRSHRRGPRAKGGPGKGPGKIPGEVSAV
                        /organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
note="chemically treated genomic DNA (Homo sapiens)"
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Eutheria; Cetartiodactyla; Tylopoda; Camelidae; Lama.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          of the early placental mammal radiation using Bayesian
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WO0200928.
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Nijmegen, NETHERLANDS
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1 Similarity 95.6%;
13; Conservative
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Sequence 5 from Patent WO0202809.
AX348497
AX348497.1 GI:18614532
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Epigenomics AG (DE)
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43; Conserva
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Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 885) and Chang, N.C.

1 (bases 1 to 885) and Chang, N.C.

1 (chang, N.C., Ho, T.F. and Chang, N.C.)

In vitro amplification by polymerase chain reaction of a partial In vitro amplification by polymerase chain reaction of gene encoding the third subtype of alpha-2 adrenergic receptor in the third subtype of alpha-2 adrenergic receptor the third subtype of alpha-2 adrenerg
                                                     kindly submitted 20-SEP-1990.
by A.C. chang, 20-SEP-1990.
Institute of Neuroscience St. 155, Sect II, Li-Noon St. 155, Sect II, Li-Noon Sc. Taipei, Taiwan, 11221 ROC.
Taipei, Taiwan, Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                        alpha-2 adrenergic receptor.
Homo sapiens (human)
Homo sapiens
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                                                                                                                                                                                                                                                                 Biochem. Biophys. Res. Commun. 172 (2), 817-823 (1990)
                                                                                                                                                                              Original source text: Human adult neuroblastoma DNA, clone PCRA2.

Draft entry and computer-readable sequence for [Unpublished (1990)]
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nilarity 95.6%;
Conservative
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/mol_type="taxon:32630"
/db_xref="taxon:32630"
/note="chemically treated genomic DNA (Homo sapiens)"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GI:177867
/organism="Homo sapiens"
/mol_type="genomic DNA"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 41.8; DB 6;
Pred. No. 0.03;
pred. No. 0; Mismatches 2;
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gene, partial cds.
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h
Similarity 91.7%;
44; Conservative
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1 (bases 1 to 1030)

1 (bases 1 to 1030)

1 (bases 2 to 1030)

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1 (bases 3 to 1030)

1 (bases 4 to 1030)

2 (bases 5 to 1030)

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2 (bases 8 to 1030)

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/codon_start=1
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Direct Submission
Submitted (16-MAY-2001) Microbiology
Submitted (16-MAY-1001) Theorelis vag,
Karolinska Institute, Theorelis vag,
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milarity 91.7%;
Conservative
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Pred. No. 0.036;
O; Mismatches
                                                 Score 41.6; DB 9; Pred. No. 0.036; 0; Mismatches 4
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3, Box 280, Stockholm 171 77,
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GATGAAGCTGAAGAGGAGGAGGAGGAGGAAGAGTGTGAACCCCAG 51

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HUMADRA2RA
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          HUMADRA2RA
Human alpha-2-adrenergic
M34041
M34041.1 GI:178197
                                                                                                                                                                                                                                                                     1 (bases 1 to 2072)
Au-Young, J. and Seilhamer, J.J.
Composition for the detection of signaling pathway gene expression
Patent: US 6500938-A 1181 31-DEC-2002;
Location/Qualifiers
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Sequence 1181 from patent US
AR270618
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Alpha-2 adrenergic receptor polymorphisms
Patent: WO 0179561-A 1 25-OCT-2001;
Liggett, Stephen B. (US); Small, Kersten
Location/Qualifiers
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Sequence 1 from Patent W00179561
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alpha-2-adrenergic receptor; plasma membrane protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AX350489.1 GI:18616091
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Eukaryota; Metazoa; Chordata; Catarrhini; Hominidae; Homo.

1 (bases 1 to 2072)
1 (bases 1 to 2072)
1 Lomasney, J.W., Lorenz, W., Allen, L.F., King, K., Regan, J.W.,
Yang-Feng, T.L., Caron, M.G. and Lefkowitz, R.J.
Expansion of the alpha 2-adrenergic receptor family: cloning and characterization of a human alpha 2-adrenergic receptor subtype, the gene for which is located on chromosome 2
Proc. Natl. Acad. Sci. U.S.A. 87 (13), 5094-5098 (1990)
                                                                                                                                              4 GATGAAGCTGAAGAGGAGGAGGAGGAAGAGTGTGAACCCCCAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Original source text: Human placenta DNA, clone alpha-2 C2. 
Draft entry and computer-readable sequence for [1] kindly s 
by J.W.Lomasney, 03-MAY-1990, for release after publication 
Location/Qualifiers
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                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                    /translation="MDHQDPYSVQATAAIAAITFLILFTIFGNALVILAVLTSRSLR
APQNLFLVSLAADILVATLIIPFSLAAHITFLILFTIFGNALVILAVLTSRSLR
APQNLFLVSLAADILVATLIIPFSLAABILVWHIALDVLFCTSSIVH
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RPQCKLNQEAWYILASSIGSFFAPCLIMILVYLRIYLIAKRSNRRGPRAKGGPGQGES
KQPRPDHGGALASAKLPALASVASAREVNGHSKSTGEKEEGGTPEDTGTTRALPSWAA
LPNKGQQVKEGVCGASPEDEAEEEEEEEEEEEPQAFVSVSPASACSPPLQOPGSR
VLATLBGQVLLGRGVGAIGGGWWRRADHVTREKRTTFVLAVVIGVFVLCWPFFFFSYS
LGAICPKHCKVPHGLFQFFFWIGYCNSSLNPVIYTIFNQDFRRAFRRILCRPWTQTAW
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## ALIGNMENTS

RESULT 1 ADB59041

## Predicting a toxic effect of a compound, useful in identifying toxicity markers in liver tissues or cells for drug screening and toxicity assays, comprises preparing gene expression profile of tissue or cells exposed to the compound. Toxic; toxin; gene expression profile; hepatotoxicity; liver; drug screening; toxicity assay; ds. WPI; 2003-689530/65 Mendrick 31-JAN-2002; 31-JAN-2003; 2003WO-US003194. 07-AUG-2003 WO2003064624-A2. Unidentified. Toxicity-related gene, 04-DEC-2003 ADB59041; ADB59041 standard; DNA; 828 15-MAR-2002; 15-MAR-2002; 30-DEC-2002; (GENE-) GENE LOGIC INC Á ; 2002US-00060087. ; 2002US-0364045P. ; 2002US-0364055P. ; 2002US-0436643P. Porter M, (first entry) SEQ ID Johnson K, ВP 4067. Higgs B, Castle ۶ Elashoff

The present invention relates to a method for predicting a toxic effect of a compound. The method comprises preparing a gene expression profile of a tissue or cell sample exposed to the compound, and comparing the gene expression profile to a database comprising SEQ ID 1-4925, where differential expression of the gene indicates at least one toxic effect. The method is useful for predicting at least one toxic effect of a compound, predicting hepatotoxicity or the progression of a toxic effect.

Claim 1; SEQ ID NO 4067; 1156pp; English.

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RESULT 2
AA19906
AU AA19906
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CON 18-F
XX Huma
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XW Poly
KW Cent
KW Phos
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Best Local (
                                                                                                                                                 Genotyping an alpha-2B, 2A, or 2C adrenergic receptor gene useful for determining whether an individual is at increased risk of developing disease associated with the corresponding receptor comprises detecting
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10-AUG-2000; 2000US-00636259.
19-OCT-2000; 2000US-00692077.
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                                                                                                                       polymorphic site
                                                                                                                                                                                                                                                                                                                                                                            Liggett
                                                                                                                                                                                                                                                                                                                                                                                                                                      (LIGG/)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    17-APR-2001; 2001WO-US012575
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WO200179561-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human; genotyping; alpha-2B; alpha-2A; alpha-2C; adrenergic receptor; polymorphic site; allelic variant; cardiovascular disease; central nervous system disease; adenylyl cyclase; MAP kinase activity phosphorylation; inositol phosphate; alpha-2BAR; chromosome 2; ds.
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                                                                                                                                                                                                                                                                                 2001-611728/70
)B; AAM52118.
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SMALL K M.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /product= "alpha-2BAR"
/note= "sequence is deleted for a 9 nucleotide
polymorphic site found at nucleotides 901-909 (
wildtype alpha-2BAR protein (AA199905)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Location/Qualifiers
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                                                                                                                                          vidual is at increased risk of developing a corresponding receptor comprises detecting
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The invention

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genotyping an alpha-2B,

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Kauhanen J,

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RESULT 3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CC receptor gene (I)-(III) by detecting a polymorphic site, comprising; (a) CC obtaining a sample having a polymorphic of (i) detecting a polymorphic cor alpha2C or fragment or complement of; and (b) detecting a polymorphic cor alpha2C or fragment or complement of; and (b) detecting a polymorphic cor site comprising nucleotide positions 901-909 of (I), a site comprising CC (site comprising nucleotide positions 901-90 of (IIV) or a site comprising (A) (c) (gygygygycy) or (B) (gygygygycy) at positions 961-972 of (III). The CC method may be used for genotyping an alpha2B, alpha2A or alpha2C receptor crisk of developing a disease associated with alpha2B, alpha2A or alpha2, comprising detecting a polymorphic site which correlate to disease and combinations of these. In addition, the technique may be used to predict an individual's response to an alpha2B, alpha2A, or alpha2C agonist (e.g. CC prazosin, ARC 239, rauwolscine, idazoxan, tolazoline, guanabenz, CC (intala04, BHT933 and combinations of these) or antagonist (e.g. yohimbine, CC (combinations of these) by detecting the polymorphic site and correlating combinations of these) by detecting the polymorphic site and correlating combinations of these) by detecting the polymorphic site and correlating combinations of these by detecting the polymorphic site and correlated to phosphate levels). The present sequence is that of the third coff the human alpha-2BAR variant, the sequence is of the wildtwom cene (Antagans)
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Scheinin M,
                                                                                                                                          20-OCT-2000;
                                                                                                                                                                                                                                                                                        CDS
                                                                                                                                                                                                                                                                                                                                                                              Human; cardiant; gene therapy; alpha2B-adrenoceptor; alpha2B-AR; glutamic acid repeat; intracellular loop; chromosome 2; catechol; norepinephrine; epinephrine; therapy; vascular contraction; varia; coronary artery; coronary heat disease; CHD; chronic angina pect;
                                                                            (JUVA-)
                                                                                                                                                                          26-APR-2001.
                                                                                                                                                                                                          WO200129082-A1.
                                                                                                                                                                                                                                                                                                                                        Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human alpha2B-adrenoceptor (alpha2B-AR) variant gene
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                                                                          JUVANTIA PHARMA
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                       Heinonen P, 1, Salonen JT,
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                                                                                                          99US-00422985.
                                                                                                                                                                                                                                    , "tag= a
/product= "Human alpha2B-adrenoceptor (alpha2B-AR)
variant protein"
                                                                                                                                                                                                                                                                    /*tag=
                                                                                                                                                                                                                                                                                                    Location/Qualifiers
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           Alhopuro P, K;
[, Tuomainen T,
, Valkonen V;
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Pred. No. 7.8e-05;
; Mismatches 0;
                         Karvonen
T, Lakka
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P-PSDB;

AAE00989

2001-300318/31

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RRESULT 4
AAD44388
ID AAD44
XX AAD4
XX AAD4
XX Huma
XX Huma
XX Huma
XX Huma
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OS Homo
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New DNA molecule encoding variant specific adrenoceptor protein with deletion of specific amino acids located in the third intracellular loop of the polypeptide, for treating vascular contraction of coronary
                                             WPI; 2002-667063/71
P-PSDB; AAE26633.
                                                                                                                                                                                                                                                                                                                                                        20-FEB-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human; hypertension; alpha-2B-adrenoceptor; A
hypertension; hypotensive; variant; gene; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human alpha-2B-adrenoceptor variant DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  13-DEC-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAD44388
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 3; Page 24-26; 37pp; English
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WO200266617-A1
                                                                                                                                                                                                                                                                      (JURI-)
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                                                                                                                                                                                                                                                                      JURILAB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            standard; DNA; 1344 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GAGGATGAAGCTGAAGAGGAGGAGGAGGAGGAAGAGTGTGAACCCCCAG 51
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                2002WO-FI000113
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Location/Qualifiers
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96.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "Human alpha-2B-adrenoceptor variant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0:
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Pred. No. 0.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AR;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             protein"
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                                                                     Matches
                                                                                  Query Match
Best Local
                                                                                                                                                                                          adrenoceptor (AR) protein. The methods and compositions of the invention are useful for detecting risks and targeting treatment for hypertension. The largeting the also useful for selecting for control of the largeting the antihypertensive effect of compounds. The present sequence is human alpha
                                                                                                                                                                                                                             The invention relates to a method for detecting a risk of hy determining the pattern of alleles encoding a variant alpha-adrenoceptor (AR) protein. The methods and compositions of tare useful for detecting risks and targeting treatment for h
                                                                                                                                                                                                                                                                                                                                                                   Detecting a risk of hypertension and targeting treatment in a subject by determining the pattern of alleles encoding a variant alpha-2-
                                                                                                                                     Sequence 1344 BP; 219 A; 459 C; 400 G; 266 T; 0
                                                                                                                                                                                                                                                                                                                  Disclosure; Page 24-26; 35pp; English
                                                                                                                                                                                                                                                                                                                                                    adrenoceptor.
                                                                                                                                                                          ·2B-adrenoceptor variant DNA
088
                                                                     49;
                                  μ
                                                                                    Similarity
GAGGATGAAGCTGAAGAGGAGGAAGAAGAGGAGGAGGAGTGTGAACCCCCAG
                  Conservative
                                                                                    93.7%;
96.1%;
                                                                 Score 47.8; DB Pred. No. 0.0005
                                                                     0
                                                                                    DB 6;
                                                                                                                                       U; 0 Other;
                                                                                                  Length 1344;
                                                                                                                                                                                                                                                                                  risk of hypertension
                                                                     Indels
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930
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RESULT 5
ABL32074
01ek
                                                                                30-JUN-2000;
01-SEP-2000;
                                                                                                                                               02-JUL-2001; 2001WO-EP007537.
                                                                                                                                                                                        03-JAN-2002
                                                                                                                                                                                                                                                                         Homo
                                                                                                                                                                                                                                                                                                                                   antiinflammatory; cancer; eye disease; arteriosclerosis; anaemia;
acute myeloid leukaemia; Alzheimer's disease; AIDS; epilepsy;
neurofibromatosis; rheumatoid arthritis; psoriasis; bowel disease
                                                                                                                                                                                                                                                                                                                                                                                                neuroprotective; anti-HIV; anticonvulsant; ophthalmological;
antirheumatic; antiarthritic; antidiabetic; antipsoriatic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human; immune system disease; cytosine methylation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human immune system associated gene SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  26-MAR-2002
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                                                                                                                                                                                                                                                                                                                                                                                                                                            antiarteriosclerotic;
                                         (EPIG-)
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                                                                                                                                                                                                                                                                         sapiens.
                                         EPIGENOMICS
Piepenbrock C,
                                                                              2000DE-01032529
2000DE-01043826
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (first
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                          antianaemic; cytostatic; nootropic;
Berlin K;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               antiasthmatic;
                                                                                                                                                                                                                                                                                                                                        epilepsy;
bowel disease;
                                                                                                                                                                                                                                                                                                                                      gene;
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The present invention provides a number of human immune system as genes which are modified by the methylation of cytosines. The sec can be used in the diagnosis and treatment of immune system disor including eye diseases such as retinopathy, neovascular glaucoma

arteriosclerosis,

AIDS,

epilepsy, anaemia,

acute myeloid

sequences associated Nucleic acid comprising diagnosis and treatment methylation.

fragment of of diseases

chemically modified gene, associated with abnormal

cytosine

for

WPI; 2002-130909/17

Claim 1; SEQ ID NO

47;

32pp + Sequence Listing;

German

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RESULT 6
AAD28364
          Query Match
Best Local Similarity
Matches 43; Conserv
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Best Local
                                                                                                              The invention relates to nucleic acids comprising a segment of chemically pretreated DNA of adrenergic alpha-1C-receptor gene. The invention also relates to oligonucleotides or peptide nucleic acid (PNA) oligomers useful for detecting cycosine methylations. The pretreated DNA is useful for the diagnosis or therapy of behavioural disorders, neurological disorders and cancer, in particular major depressive disorder, Tourette's syndrome, schizophrenia, psychiatric and neurological disorders, smoking, immunodeficiency virus dementia, migraine, behaviours in schizophrenic and schizopaffective patients, and suicidal behaviour in patients with schizophrenia. The nucleic acid is useful for detecting the methylation state of all CpG dinucleotides and/or single nucleotide polymorphisms (SNPs). The present sequence is human chemically treated genomic DNA
                                                                                           Sequence
                                                                                                                                                                                                                                                                                                                                                                                                           Claim 1; Page 40-44; 190pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2002-154759/20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Olek A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        30-JUN-2000; 2000DE-01032529.
01-SEP-2000; 2000DE-01043826.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             segment
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human; cytostatic; antidepressant; neuroleptic; nootropic; antiaddictive; adrenergic alpha-1C-receptor; cytosine methylation; therapy; alcoholism; behavioural disorder; neurological; psychiatric; cancer; schizophrenia; Tourette's syndrome; smoking; human immunodeficiency virus dementia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   02-JUL-2001; 2001WO-EP007540.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (EPIG-)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human chemically treated genomic DNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                rheumatoid
                                                                                                                                                                                                                                                                                                                                                                                                                                                         nucleic acid useful for diagnosis and therapy of behavioral der, neurological disorder and cancer, comprises a sequence of a sequence of a chemically pretreated DNA of adrenergic alpha-1C-receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                5880
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              abuse; migraine;
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                                                                                           6904
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EPIGENOMICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Piepenbrock
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43; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GAGGATGAAGCTGAAGAGGAGGAGGAGGAGGAGGAAGAGTGTGAA 45
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           d arthritis,
The present
                                                                                BP; 1244 A; 314 C; 2303 G;
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                           82.0%;
95.6%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           entry)
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95.6%;
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    Score 41.8; DI
Pred. No. 0.02
0; Mismatches
          <u>,</u>
                                                                                                                                                                                                                                                                                                                                                                                                             English.
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Pred. No. 0
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                       DB 6;
.025;
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                                          Length 6904;
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    Indels
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Gaps
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RESULT 7
AAI 9905
XX AAI 9
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X
The invention relates to genotyping an alpha-2B, 2A, or 2C adrenergic CC receptor gene (I)-(III) by detecting a polymorphic site, comprising; (a) obtaining a sample having a polymorlectide encoding an alpha-2B, alpha2A or alpha2C or fragment or complement of; and (b) detecting a polymorphic CC site comprising nucleotide positions 901-909 of (I), a site comprising (CC cytosine or guanine at position 753 of (IIV) or a site comprising (A) (19939939930) or (B) (9939939339) at positions 961-972 of (III). The CC gene and further used to determine whether an individual is at increased CC comprising detecting a polymorphic site which correlate to disease associated with alpha2A or alpha2A or alpha2C receptor CC comprising detecting a polymorphic site which correlate to disease and CC compinations of these. In addition, the technique may be used to predict compinations of these. In addition, the technique may be used to predict compinations of these. In addition, the technique may be used to predict compinations of these. In addition, the technique may be used to predict compinations of these or an alpha2B, alpha2A, or alpha2C agonist (e.g. CC UK14304, BHT933 and combinations of these) or antagonist (e.g. yohimbine,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         밁
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Genotyping an alpha-2B, 2A, or 2C adrenergic receptor gene useful for determining whether an individual is at increased risk of developing a disease associated with the corresponding receptor comprises detecting
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 4; Page 144; 163pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           polymorphic site.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           P-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            17-APR-2000; 2000US-00551744
10-AUG-2000; 2000US-00636259
19-OCT-2000; 2000US-00692077
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (SMAL/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (LIGG/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human alpha-2BAR third intracellular loop encoding DNA
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DB; AAM52117.
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SMALL K M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 GAGGATGAAGCTGAAGAGGAGGAGGAGGAGGAGGAGGAGTGTGAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Small KM
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/note= "sequence includes a 9
at nucleotides 901-909 absent
(AAI99906)"
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Query Match
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Scheinin M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human; cardiant; gene therapy; alpha2B-adrenoceptor; alpha2B-AR; glutamic acid repeat; intracellular loop; chromosome 2; catecholamine norepinephrine; epinephrine; therapy; vascular contraction; coronary artery; coronary heat disease; CHD; chronic angina pectoris; acute myocardial infarction; AMI; Prinzmetal's variant; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 prazosin, ARC 239, rauwolscine, idazoxan, tolazoline, phentolamine and combinations of these) by determine the polymorphic site and correlating the site to a predetermined response (where the response is correlated to adenylyl cyclase, MAP kinase activity, phosphorylation or inositol phosphate levels). The present sequence is that of the third intracellular loop of the human alpha-2BAR (GenBank Accession AF009500), the sequence includes a 9 nucleotide polymorphic site at nucleotides 901-909, absent in the alpha-2BAR variant (AAI99906)
                                                                                                                  New DNA molecule encoding variant specific adrenoceptor protein with deletion of specific amino acids located in the third intracellular loop of the polypeptide, for treating vascular contraction of coronary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 1353 BP;
                                                                            Disclosure; Page 27-29; 37pp;
                                                                                                                                                                                                           Salonen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       04-JUL-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAD04762 standard;
                            (amino acide
                                                                                                                                                                                                                                                              (JUVA-) JUVANTIA PHARMA LTD OY
                                           (alpha2B-AR)
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2001-300318/31.
DB; AAE00990.
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                                                                                                                                                                                                                                    Heinonen P,
                                                                                                                                                                                                            Kauhanen
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llarity 91.7%;
Conservative
                                                                                                                                                                                                                        Salonen
                                                                                                                                                                                                                                                                                                                 2000WO-FI000913
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                                                                                                                                                                                                                                                                                        99US-00422985.
                                                                                                                                                                                                                                                                                                                                                                                          /*tag= a
/product= "Human alpha2B-adrenoceptor
protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                             Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DNA;
                                                                                                                                                                                                           'n,
                                                                                                                                                                                                           Alhopuro P, Ka
, Tuomainen T,
Valkonen V;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1353
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Pred. No. 0
                                                                            English.
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                                                                                                                                                                                                                       Karvonen
T, Lakka
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                                                                                                                                                                                                                       Koulu M, P
Nyyssoenen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; alpha2B-AR; ; 2; catechol:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Other;
                                                                                                                                                                                                                                                                                                                                                                                                         (alpha2B-AR)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      catecholamine;
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Query Match Best Local Similarity

81.6%; 91.7%;

Score 41.6; Pred. No. 0

DB 6;

Length 1353;

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Best Local S
Matches 44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Alpha2-AR mediate many of the physiological effects of the catecholamines, norepinephrine and epinephrine. An antagonist of alpha2 adrenoceptor is useful for treating a mammal suffering from vascular contraction of coronary arteries and a disease involving vascular contraction of coronary arteries which is clinically expressed as coronary heat disease (CHD), unstable chronic angain pectoris which is clinically expressed as Prinzmetal's variant form or acute myocardial infarction (AMI). Alpha2B-AR gene is used in gene therapy
                                   The invention relates to a method for detecting a risk of hypertension by determining the pattern of alleles encoding a variant alpha-2B-adrenoceptor (AR) protein. The methods and compositions of the invention are useful for detecting risks and targeting treatment for hypertension. The kit is also useful for selecting for clinical drug trials testing the antihypertensive effect of compounds. The present sequence is human alpha
                                                                                                                                                                           Detecting a risk of hypertension and targeting treatment in a subject determining the pattern of alleles encoding a variant alpha-2-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAD44389;
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                                                                                                                                  Disclosure; Page 27-29; 35pp; English
                                                                                                                                                                                                                                  WPI;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human alpha-2B-adrenoceptor gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      13-DEC-2002
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                                                                                                                                                                                                                     P-PSDB;
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                                                                                                                                                                                                                                                                                                                                        13-FEB-2002; 2002WO-FI000113.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human; hypertension; alpha-2B-adrenoceptor; AR; antihypertensive; hypertension; hypotensive; gene; ds.
                            2B-adrenoceptor
                                                                                                                                                                                                                                2002-667063/71.
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/product= "Human alpha-2B-adrenoceptor
                                                                                                                                                                                                                                                                                                                                                                                                                                    /*tag=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Location/Qualifiers
  223
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  A; 459
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Pred. No. 0
    405
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 G.
  266 T; 0
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    0 Other;
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RESULT 10
AAQ14151
ID AAQ14
RESULT 11
AAT59499
ID AAT59
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AC AAT59
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DT 25-MP
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Matches 44
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             06-JAN-1992
                                                                                                                                                                                                                                                       Clone NGC-alpha2beta was isolated from a human spleen genomic screening with a fragment of the human 5-HTIA receptor gene. To be used to express recombinant receptor protein which can be uproduce antibodies for inhibition of receptor function
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US5053337-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Neurotransmission;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human alpha 2 beta adrenergic receptor gene
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAQ14151 standard; DNA; 2064 BP
                                                                           AAT59499;
                                                                                                                                                                                                                                   Sequence 2064 BP;
                                                                                                                                                                                                                                                                                                           Claim 1; Fig 2; 15pp; English.
                                                                                                                                                                                                                                                                                                                                                                                            Weinshank RL;
                                                                                                                                                                                                                                                                                                                                                                                                                                      30-OCT-1989;
                                                                                                                                                                                                                                                                                                                                                                                                                                                          30-OCT-1989;
  Alpha-2b adrenergic receptor; adrenoceptor; adrenaline; epinephrine;
                      Human alpha-2b adrenergic receptor genomic DNA clone
                                                                                                                                                                                                                                                                                                                               Isolated DNA encoding human adrenergic receptor -
acids encoding alpha, 2-beta adrenergic receptor,
                                                                                              AAT59499 standard; DNA; 2064 BP.
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                                                                                                                                                  1290
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                                                                                                                                                                  GATGAAGCTGAAGAGGAGGAGGAGGAGGAGGAGAGTGTGAACCCCCAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
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                                           (revised)
(first en
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                                                                                                                                                                                                                                                                                                                                                                                                                                      89US-00428856
                                                                                                                                                                                                                                                                                                                                                                                                                                                           89US-00428856
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Location/Qualifiers 288. .1752
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /*tag=
                                                                                                                                                                                                                                    319 A; 696 C; 659 G; 390 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      adrenaline; epinephrine; NGC-alpha2beta; ss
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             entry)
                                            entry)
                                                                                                                                                                                                    81.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ٥,
                                                                                                                                                                                           0
                                                                                                                                                                                          Score 41.6; DB Pred. No. 0.027; Mismatches
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                                                                                                                                                                                                              DB 2;
                                                                                                                                                                                            4.
                                                                                                                                                                                                               Length 2064;
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                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                for detecting for screening
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           939
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                                                                                                                                                                                                                                                                                                                                nucleic
drugs.
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RESULT 12
ACA56583
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                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local S
Matches 44
                                                                                                                                                                                                                                                                                                                                                                                                                                                    A genomic DNA clone (AAT59499) codes for human alpha-2B adrenergic receptor (AAW11804), a member of the rhodopsin-like signal transducer family. It was isolated from a human spleen genomic library in the lambda vector Charon 28 by screening with a 1.6 kb fragment of the human 5-hydroxytryptamine receptor gene. Plasmid pNGC-alpha-2B comprising DNA encoding the alpha-2B adrenceptor is deposited as ATCC 68144. Vectors have been adapted to allow prodn. of alpha-2B adrenceptor in bacterial, yeast or mammalian cells; transfected Ltk- cells, designated L-NGC-alpha-2B, are deposited as ATCC CRL 10275. Membranes of such cells can used in novel methods to identify drugs which specifically interact with, and bind to, the alpha-2B adrenergic receptor. (Updated on 25-MAR-2003 to correct PF field.)
                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 2064 BP; 319 A; 696 C; 659 G; 390 T; 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Disclosure; Fig 2A-E; 16pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     expressing recombinant receptor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Assay for alpha-2b adrenergic receptor ligands - using membranes of cells
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               30-OCT-1989;
30-MAY-1991;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     21-JAN-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US5595880-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            signal transduction; neurotransmitter; ligand; ss.
                                                                                            Human; probe; ss; array element; Parkinson's disease; signalling pathway population; cancer; adenocarcinoma immunopathy; AIDS; asthma; neuropathy; Alzheimer's di
                                                                                                                                                     Human signalling pathway polynucleotide probe SEQ ID NO
                                                                                                                                                                                                               ACA56583;
                                                                                                                                                                                                                                          ACA56583 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 1997-107576/10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (SYNA-) SYNAPTIC PHARM CORP
                                         US6500938-B1
                                                                    Ното
                                                                                                                                                                                   06-JUN-2003
                                                                                                                                                                                                                                                                                                                1290
                                                                  sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PR,
                                                                                                                                                                                                                                                                                                                                                                     44;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAW11804
                                                                                                                                                                                                                                                                                                                                                                                    Similarity
                                                                                                                                                                                                                                                                                                                                     GATGAAGCTGAAGAGGAGGAGGAGGAGGAGGAGGAGTGTGAACCCCAG
                                                                                                                                                                                                                                                                                                                GAAGAGGAGGAAGAGGAGGAGGAGGAAGAGTGTGAACCCCAG
                                                                                                                                                                                                                                                                                                                                                                     81.6%; Score 41.6; DB 2; llarity 91.7%; Pred. No. 0.027; Conservative 0; Mismatches 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Weinshank
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91US-00707604
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Location/Qualifiers
288. .1751
/*tag= a
                                                                                                                                                                                                                                          CDNA; 2072
                                                                                                                                                                                     entry)
                                                                                                               adenocarcinoma; leukaemia;
                                                                                                                                                                                                                                                                                                                                                                       4.
                                                                                                                                                                                                                                                                                                                                                                                                Length 2064;
                                                                                                                                                                                                                                                                                                                                                                                                                              U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                 disease; microarray.
                                                                                                                                                                                                                                                                                                                   1337
                                                                                                                                                                                                                                                                                                                                                                       0;
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30-JAN-1998;

98US-00016434

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local
                                                                          G protein-coupled receptor; GPCR; antigenic peptide; gene therapy; growth-related disease; cell regeneration-related disease; growth-related disease; cell regeneration-related disease; AIDS; cancer; immunological-related cell proliferative disease; autoimmune disease; Alzheimer's disease; atheroselerosis; infection; osteoarthritis; allergy; osteoporosis; cardiomyopathy; inflammation; Crohn's disease; dabettes; graft versus host disease; Parkinson's disease; multiple sclerosis; pain; psoriasis; anxiety; depression; schizophrenia; dementia; memory loss; mental retardation; epilepsy; asthma; tuberculosis; obesity; nausea; hypertension; hypotension; renal disorder; rheumatoid arthritis; trauma;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Combination of polynucleotide probes, useful as array elements microarray for monitoring the expression of a number of target polynucleotides.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The invention relates to a combination which, comprises a number of polynucleotide probes comprising a sequence selected from one of the 1490 sequences mentioned in the specification. The combination is useful as an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 1; SEQ ID NO 1181; 65pp; English.
                                                   ulcer; gene;
                                                                                                                                                                                                                                                                                                                                                                                   Human alpha 2b-adrenoceptor nucleotide SEQ ID NO:41.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ABZ42624 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        seqdata.uspto.gov/sequence.html?DocID=06500938B1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (INCY-) INCYTE GENOMICS INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            30-JAN-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1304
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             44;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2072 BP; 316 A; 705 C; 660 G; 391 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GAAGAGGAGGAAGAGGAGGAGGAGGAAGAGTGTGAACCCCAG 1351
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GATGAAGCTGAAGAGGAGGAGGAGGAGGAAGAGTGTGAACCCCAG 51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                          (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            98US-00016434
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    81.6%;
91.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 41.6;
Pred. No. 0.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0;
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Homo sapiens

AAD06932
ID AAD0
XX
AC AAD0
XX
O6-A
XX
O6-A
XX
VACC
XX
VACC
XX
VACC
XX

06-AUG-2001 AAD06932;

(first entry)

AAD06932 standard; cDNA; 593

0

Human; melanoma tumour-associated antigen; vaccine; cancer; immune response; metastati

antigen; cytostatic; gene therapy;
metastatic melanoma; immunotherapy; ss.

3' end of human melanoma tumour-associated antigen cDNA from clone 5.31.

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                               S
                                                                                                                                                                                         The present invention describes antigenic peptides (I) comprising: (a) cany one of 1601 sequences (see ABP82019 to ABP83619) of 12-24 amino CC acids. Also described: (I) an assay for the detection of a particular GC protein-coupled receptor (GPCR) or a candidate polypeptide in a sample; CC and (2) an isolated antibody having high specificity and high affinity or CC avidity for a particular GPCR. (I) can be used as GPCR modulators and in CC gene therapy. The antigenic peptides for GPCRs are useful in detecting an attibody against a particular GPCR, and in the production of specific CC antibodies. The peptides and antibodies are also useful for detecting the CC presence or absence of corresponding GPCRs. The antigenic peptides for CPCRs and antibodies are useful for diagnosing and designing drugs for CC treating immune-related diseases, growth-related diseases, cell CC diseases, or autoimmune diseases, erouth-related cell proliferative CC diseases, or autoimmune diseases, e.g. AIDS, Alzheimer's disease, CC atherosclerosis, bacterial, fungal, protozoan or viral infections, catherosclerosis, bacterial, fungal, protozoan or viral infections, CC anxiety, depression, schizophrenia, dementia, mental retardation, memory CC loss, epilepsy, asthma, tuberculosis, obesity, nausea, hypertension, cc and other disorder in which GPCRs are involved. The antibodies may be cused in immunoassays and immunodiagnosis. ABZ42523 to ABZ42869 encode CC GPCR proteins given in ABP81675 to ABB82018, which are used in the code code CC GPCR proteins of the present invention
                                                                            Best Loc
Matches
                                                                                                 Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Disclosure; Fig 1; 523pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   autoimmune diseases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New isolated antigenic peptides e.g., for G protein-coupled receptors (GPCR), useful for diagnosing and designing drugs for treating conditions in which GPCRs are involved, e.g. AIDS, Alzheimer's disease, cancer or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Burmer GC, Roush CL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   19-DEC-2000; 2000US-0257144P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          19-DEC-2001; 2001WO-US050107.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  08-AUG-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WO200261087-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (LIFE-) LIFESPAN BIOSCIENCES INC
                                                                              44;
                         4 GATGAAGCTGAAGAGGAGGAGGAGGAGGAGAGAGTGTGAACCCCCAG 51
GAAGAGGAAGAAGAGGAGGAGGAGGAGGAGGAGGTGTGAACCCCAG
                                                                                                                                                               3274 BP;
                                                                              Conservative
                                                                                                                                                               587 A; 979 C; 967 G; 741 T; 0 U; 0 Other;
                                                                                               81.6%;
91.7%;
                                                                            0;
                                                                                                 Score 41.6; DB 7;
Pred. No. 0.028;
                                                                                Mismatches
                                                                              4
                                                                                                                     Length 3274;
                                                                                Indels
  939
                                                                                <u>.</u>
                                                                              Gaps
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Homo sapiens

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 23-APR-2001;
27-APR-2001;
05-JUN-2001;
09-JUL-2001;
31-AUG-2001;
                                                                                23-APR-2002;
                                                                                                                                    WO200286090-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The present sequence is 3' end cDNA of clone 5.31 encoding human melanoma tumour-associated antigen. The cDNA is useful in gene therapy and as an oligonucleotide probe for detecting mRNA coding for the melanoma tumour-associated antigen in a sample. The cDNA is useful for vaccinating an individual who is at risk of getting cancer, suspected of having cancer or has cancer. The present sequence is useful for inhibiting growth of tumour-associated antigen is useful for detection, diagnosis and staging tumour-associated antigen is useful for detection, diagnosis and staging immunotherapy. The identification of novel tumour antigens may allow recurrence and metastatic disease to be detected and disease burden monitored. Characterisation of the melanoma tumour-associated antigen is
                                                                                                                                                            Aspergillus fumigatus.
                                                                                                                                                                                     cancer; contamination;
                                                                                                                                                                                                                      Aspergillus fumigatus essential gene #2614.
                                                                                                                                                                                                                                                      16-APR-2003
                                                                                                                                                                                                 Fungicide; cytostatic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 593 BP; 158 A; 115 C; 146 G; 174 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   of particular use in melanoma research
                                                                                                                                                                                                                                                                                                       ABT20256 standard; DNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Isolated DNA sequence encoding a melanoma tumor associated antigen, useful for detection, diagnosis and staging of melanomas, monitoring metastatic melanomas and as a target for immunotherapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim
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                                                                                                                                                                                                                                                                                                                                                                                                                            42;
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                                                                                                                                                                                                                                                                                                                                                                                                                                       Similarity
                                                                                                                                                                                                                                                                                                                                                                 GAGGAGGAGGAAGATGAGGAGGACGAAGGAAGAAGAGAGTGAACCTCAG 345
                                                                                                                                                                                                                                                                                                                                                                                         GAGGATGAAGCTGAAGAGGAGGAGGAGGAGGAGGAAGAGTGTGAACCCCCAG 51
; 2001US-0285697P.
; 2001US-0287066P.
; 2001US-0295890P.
; 2001US-0303899P.
; 2001US-0316362P.
                                                                               2002WO-US013142.
                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                   (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   99US-0160042P
                                                                                                                                                                                                                                                                                                                                                                                                                                    71.8%;
82.4%;
                                                                                                                                                                           essential gene; Aspergillus fumigatus; infection; biofilm; antibody; immune response; ds.
                                                                                                                                                                                                                                                                                                       2367
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                                                                                                                                                                                                                                                                                                                                                                                                                         0;
                                                                                                                                                                                                                                                                                                       ВÞ
                                                                                                                                                                                                                                                                                                                                                                                                                      Pred. No. 0.500; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 36.6;
Pred. No. 0.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB
                                                                                                                                                                                                                                                                                                                                                                                                                                              4; Length 593;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                      9;
                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                     0,
                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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Search completed: March Job time: 268.5 secs

2

2004,

05:39:01

밁 S

2314 GAGGAGGAAGAAGAAGAGGAGGAAGAAGAAGAGTTTGA

GAGGATGAAGCTGAAGAGGAGGAGGAGGAGGAAGAGTGTGA 44

Matches Query Match

39;

Conservative

0,

5 -

Gaps

0;

Similarity

70.6%; 88.6%;

Score 36; DB Pred. No. 0.87 0; Mismatches

DB 7;

Length 2367; Indels

Sequence 2367 BP; 630 A; 644 C; 681 G;

412 T; 0 U; 0 Other;

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CC subject (e.g. cancer), to prevent or inhibit formation of an object (c) by A. funigatus, or to prevent or inhibit formation on a surface of a content content content of an object (c) biofilm comprising A. funigatus. The polynucleotides are useful for coxpressing recombinant protein for characterisation, screening or corganisms invade or reside, for comparing with the pathogenic corganisms invade or reside, for comparing with the buA sequence of A. CC funigatus to identify duplicated genes or paralogues having the same or sequences of other related or distant pathogenic organisms to identify and/or function, for comparing with DNA cc sequences of other related or distant pathogenic organisms to identify potential orthologous essential or virulence genes, for selecting and comparing of other related or distant pathogenic organisms to identify of expression patterns, for raising anti-protein antibodies, as an cc antigen to raise anti-DNA antibodies or to elicit another immune cc with which binding occurs or to identify inhibitors of the binding cc determine levels of the protein in biological fluids, as a marker for comparine levels of the protein in biological fluids, as a marker for isolate correlative receptors or ligands in the case or virulence cc factors. This polynucleotide sequence represents one of the essential xxx.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       organism such subject (e.g.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The invention relates to novel purified or isolated nucleic acids of essential genes of Aspergillus fumigatus. The isolated nucleic acids the invention are used to treat or prevent infections by a pathogenian
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New purified or isolated nucleic acids of essential genes of Aspergillus fumigatus, useful for treating or preventing infections by A. fumigatus, or for treating a non-infectious disease in a subject e.g. cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Disclosure; Page; 175pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Jiang B,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (ELIT-) ELITRA PHARM INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Tishkoff D,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      sed to treat or prevent infections by a pathogenic funigatus, to treat a non-infectious disease in a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Zamudio C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eroshkin
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Title:
Perfect score:
Sequence:
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No.
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           OM nucleic - nucleic search, using sw model
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                            Score
     seq length: 0
seq length: 2000000000
                                                                                                                                                                                                                                                                                                                                                                                            Query
Match
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Gapop 10.0 , Gapext 1.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   March 2, 2004, 05:39:14; Search time 60 Seconds (without alignments) 471.708 Million cell updates/sec
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                 Issued_Patents NA:*

1: /cgn2_6/ptodata/2/ina/5A_COMB.seq:*

2: /cgn2_6/ptodata/2/ina/5B_COMB.seq:*

3: /cgn2_6/ptodata/2/ina/6A_COMB.seq:*

4: /cgn2_6/ptodata/2/ina/6B_COMB.seq:*

5: /cgn2_6/ptodata/2/ina/PCTUS_COMB.seq:*

6: /cgn2_6/ptodata/2/ina/backfiles1.seq:*
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                 Length
                                                                                                                                                                                                                                                                                                                                                                                            DB
US-09-016-434-1181
US-09-0915-38A-12
PCT-US94-09752-1
US-08-094-948A-4
PCT-US96-09319-4
US-09-621-976-18769
US-09-621-976-18769
US-09-620-312D-1085
US-09-634-9457-1668
US-09-634-457-1668
US-09-634-457-1668
US-09-634-1248-1668
US-09-637-1325-1668
US-09-637-1325-1668
US-09-357-014-8
US-09-3582-4
US-09-345-882-1
US-09-345-882-1
US-09-345-882-1
US-09-345-882-1
US-09-345-882-1
US-09-705-309
US-09-614-1248-309
US-09-614-1248-309
US-09-614-1248-309
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                                                    Sequence 1085, Ap
Sequence 1, Appli
Sequence 1668, Ap
Sequence 1668, Ap
Sequence 1668, Ap
Sequence 1668, Ap
Sequence 21, Appli
Sequence 8, Appli
Sequence 6, Appli
Sequence 6, Appli
Sequence 4, Appli
Sequence 1, Appli
Sequence 1, Appli
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Sequence 12, Appli
Sequence 1, Appli
Sequence 4, Appli
Sequence 4, Appli
Sequence 33, Appli
Sequence 18769, Appli
Sequence 1085, Appli
Sequence 1085, Appli
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Query Best	RESULT US-09-1 Sequel Fates Fa	C C C C C C C C C C C C C C C C C C C
uery Match 81.6%; Score 41.6 est Local Similarity 91.7%; Pred. No.	Quence 1181, Application US/0901643 tent No. 650038 ENERAL INFORMATION: APPLICANT: Janice Au-Young APPLICANT: Jeffrey J. Seilhamer ITILE OF INVENTION: COMPOSITION F ITILE OF INVENTION: PATHWAY GENE UNMER OF SEQUENCES: 1490 CORRESPONDENCE ADDRESS: ADDRESSEE: INCYTE PHARMACEUTICA STREET: 3174 PORTER DRIVE CITY: PALO ALTO STATE: CALIFORNIA COUNTRY: USA ZIP: 94304 COMPUTER: READABLE FORM: MEDIUM TYPE: Floppy disk COMPUTER: IBM PC COMPATIBLE COMPUTER: IBM PC COMPATIBLE OPERATION TYPE: Floppy disk COMPUTER: BAD ACTON DATA: APPLICATION NUMBER: US/09/016,4 FILING DATE: HEREWITH CLASSIFICATION: APPLICATION DATA: APPLICATION NUMBER: US/09/016,4 FILING DATE: FILING DATE: FILING DATE: FILING DATE: APPLICATION DATA: APPLICATION NUMBER: 37,071 REFERENCE/DOCKET NUMBER: PA-000 TELECOMMUNICATION INFORMATION: ATTORNEY/AGENT INFORMATION: ATTORNEY/AGENT INFORMATION: ATTORNEY/AGENT INFORMATION: APPLICATION UNMBER: 37,071 REFERENCE/DOCKET NUMBER: PA-000 TELECOMMUNICATION INFORMATION: ATTORNEY/AGENT INFORMATION: ATTORNEY/AGENT INFORMATION: APPLICATION INFORMATION: TELEPAX: (650) 855-0555 TELEPAX: (650) 855-0556 TELEPAX: 650) 854-4166 NFORMATION FOR SEQ ID NO: 1181: SEQUENCE CHARACTERISTICS: LENGTH: 2072 base pairs TYPE: nucleic acid STRANDEDNESS: single TOPOLOGY: linear IMMEDIATE SOURCE: LIBRARY: GENBANK CLONE: 9178197 9-016-434-1181	8 31.2 61.2 129 4 US-09-589- 9 31.2 61.2 403 4 US-09-621- 1 31.2 61.2 438 4 US-09-702- 2 31.2 61.2 438 4 US-09-716- 3 31.2 61.2 438 4 US-09-614- 3 31.2 61.2 438 4 US-09-614- 3 31.2 61.2 438 4 US-09-621- 5 31.2 61.2 450 4 US-09-621- 6 31.2 61.2 452 4 US-09-621- 7 31.2 61.2 458 4 US-09-621- 8 31.2 61.2 459 4 US-09-621- 9 31.2 61.2 459 4 US-09-621- 1 31.2 61.2 464 4 US-09-621- 2 31.2 61.2 464 4 US-09-621- 3 31.2 61.2 466 4 US-09-621- 3 31.2 61.2 521 4 US-09-621- 3 31.2 61.2 521 4 US-09-621- 3 31.2 61.2 521 4 US-09-621- 3 31.2 61.2 686 4 US-09-621- 4 31.2 61.2 686 4 US-09-621- 5 31.2 61.2 686 4 US-09-621-
; DB 4; Length 2072; 0.0014;	OR THE DETECTION OF SIGNALING EXPRESSION LS, INC. Windows/MS-DOS 6.2 34	184-309 Sequence 309, App 976-18731 Sequence 18731, A 705-1028 Sequence 1028, App 457-1028 Sequence 1028, App 457-1028 Sequence 1028, App 325-1028 Sequence 1028, App 976-3667 Sequence 1028, App 976-1227 Sequence 1227, App 976-1223 Sequence 1227, App 976-1239 Sequence 1227, App 976-18757 Sequence 18757, App 976-18757 Sequence 18757, App 976-18761 Sequence 18757, App 976-18761 Sequence 18757, App 976-18762 Sequence 18757, App 976-18763 Sequence 18757, App 976-18763 Sequence 18757, App 976-18772 Sequence 9, Appli

В

Matches

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RESULT 3
PCT-US94-09752-1
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FEATURE:
OTHER INFORMATION: 3' end of clone 5.31 encoding a
OTHER INFORMATION: tumor-associated antigen
US-09-691-538A-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 1, Application PC/TUS9409752
GENERAL INFORMATION:
APPLICANT: David S. Strayer and Avinash Chander
TITLE OF INVENTION: Compositions and Methods for
TITLE OF INVENTION: Targeting Cells and Modulating Pulmonary Surfactant Secretion
                                                         PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/176,218
FILING DATE: December 30, 1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/114,951
FILING DATE: August 31, 1993
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CURRENT APPLICATION NUMBER: US/09/691,538A CURRENT FILING DATE: 2000-10-18 PRIOR APPLICATION NUMBER: US 60/160,042 PRIOR FILING DATE: 1999-10-18 NUMBER OF SEQ ID NOS: 12 SEQ ID NO 12 LENGTH: 593
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                  CORPUTER: IBM PS/2
OPERATING SYSTEM: PC-DOS
SOFTWARE: WORDPERFECT 5.1
CURRINT APPLICATION DATA:
TOTAL TRANSPORTED DATA:
                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 Mb
MEDIUM TYPE: STORAGE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Strong, Theresa
APPLICANT: Conry, Robert M.
APPLICANT: LoBuglio, Albert F.
TITLE OF INVENTION: Melanoma Antigens and Methods
FILE REFERENCE: D6253
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CORRESPONDENCE ADDRESS:
ADDRESSEE: Jane Massey Licata, Esq.
STREET: 210 Lake Drive East, Suite 201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STREET: 210 DEC. CITY: Cherry Hill STATE: NJ
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                                                                                                                                                                                                                                               APPLICATION NUMBER: FILING DATE: Herew: CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1304 GAAGAGGAGGAAGAAGAAGAAGAAGAAGAAGAAGAAAAACCCCAAG 1351
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GATGAAGCTGAAGAGGAGGAGGAGGAGGAGGAGGAGAGTGTGAACCCCAG
                                           Маввеу
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                                                                                                                                                                                                                                                                  Herewith
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Pred. No. 0.033;
0; Mismatches 9; Indels
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                                                                                                                               US-08-094-948A-4
             Query Match 67.1%;
Best Local Similarity 83.0%;
Matches 39; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: US/08/094,948A
FILING DATE: 21-UULY-1993
PRIOR APPLICATION DATA: 07/643,982
APPLICATION NUMBER: US 07/643,982
FILING DATE: 18-UAN-1991
ATTORNEY/AGENT INFORMATION:
NAME: Myers, Louis (PLM)
REGISTRATION NUMBER: JDP-013DV
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)227-7400
TRILEPHONE: (617)227-7400
                                                                                                                                                                                                                                                                                                                                                   TELEFAX: (617)227-5941
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PCT-US94-09752-1
                                                                                                                                                  FEATURE:
NAME/KEY:
LOCATION:
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J8-Uy.
Pacquence 4, Ab-
Patent No. 5621075
Patent No. 5621075
Patent No. 5621075
Patent No. 5621075
Patent No. 621075
Patent No. 62
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                                                                                                                                                                                                                              MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Kahn, C. Ronald
APPLICANT: White, Morris F.
APPLICANT: Rothenberg, Paul Louis
TITLE OF INVENTION: INSULIN RECEPTOR SUBSTRATE
NUMBER OF SEQUENCES, 29
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEFAX: (609) 779-8488 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                    TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                         TOPOLOGY:
                                                                                                                                                                                                                                                                                                                             LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REGISTRATION NUMBER: 32,257
REFERENCE/DOCKET NUMBER: JE:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (609) 779-2400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE CHARACTERISTICS:
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STRANDEDNESS: single stranded
TOPOLOGY: linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    572 GAAGATGATGATGAAGAGGAGGAGGAAGAAGAAGAATGTG 614
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 Similarity
38; Conserv
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                                                                                                                                                                                                                                                                                                                   5125 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Massachusetts
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Application US/08094948A
                                                                                                                                                                                                                                                                                                                                                                                            (617) 227-5941
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      60 State Street,
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                                                                                                                                                                                                                                                    linear
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        Score 34.2; DB
Pred. No. 0.19;
0; Mismatches
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                                                      DB 1;
        8;
                                                      Length 5125;
     Indels
     0
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0
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295

Matches

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Sequence 333, Application US/09328111
Patent No. 6262333
GENERAL INFORMATION:
APPLICANT: Endege, Wilson O.
APPLICANT: Steinmann, Kathleen E.
APPLICANT: Buthes, Jon H.
APPLICANT: Buthes, Christopher C.
APPLICANT: Bushnell, Steven E.
APPLICANT: Carroll III, Eddie
                                                                                                                                                               RESULT 6
US-09-328-111-333
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PCT-US96-09319-4
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                                                                                                                                                                                                                                                                                                               Matches
                                                                                                                                                                                                                                                                                                                                               Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEFAX: (617)227-5941
[NFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: Myers, Louis (PLM)
REGISTRATION NUMBER: 35,965
REGERENCS/DOCKET NUMBER: JDI
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)227-7400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: PatentIn Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQUENCES: 29
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lahive & Cockfield
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Kahn, C. Ronald
APPLICANT: White, Morris F.
APPLICANT: Rothenberg, Paul Louis
TITLE OF INVENTION: INSULIN RECEPTOR SUBSTRATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                          MOLECULE TYPE: cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: US 08/094,948
FILING DATE: 21-JULY-1993
APPLICATION NUMBER: US 07/643,982
FILING DATE: 18-JAN-1991
TTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                        NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH: 5125 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                       LOCATION:
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                                                                                                                                                                                                                                                            3 GGATGAAGCTGAAGAGGAGGAGGAGGAGGAGGAGGAGGTGTGAACCCCC 49
                                                                                                                                                                                                                                                                                                                               Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (617) 227-5941
TD NO: 4:
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589..4053
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83.0%;
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APPLICANT:

Hosken, Nancy Ann
Craig H. Day
Davin C. Dillon
McGowan, Patrick
Sleath, Paul R.

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                                                 US-09-894-998A-34/c
                                                                     RESULT 8
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SOFTWARE: Patent.pm
SEQ ID NO 18769
GENERAL
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Best Local S
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SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 333
                                Sequence
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GENERAL INFORMATION:
                Sequence 34, Application US/09894998A Patent No. 6537555
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                                                                                                                                                                                                                                                                                                                                                                                  FILE REFERENCE: GENSET.054PR2
CURRENT APPLICATION NUMBER: US/09/621,976
CURRENT FILING DATE: 2000-07-21
                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Giordano, J.Y. TITLE OF INVENTION: ESTs and Encoded Human Proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Ford, Donna M.
APPLICANT: Lewis, Marcia E.
APPLICANT: Monahan, John E.
APPLICANT: Schlegel, Robert
APPLICANT: Schlegel, Robert
TITLE OF INVENTION: NOVEL HUMAN GENES AND GENE EXPRESSION
TITLE OF INVENTION: PRODUCTS
FILE REFERENCE: CCD-257 (US)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EARLIER APPLICATION NUMBER: US 60/088,801 EARLIER FILING DATE: 1998-06-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CURRENT APPLICATION NUMBER: US/09/328,111
CURRENT FILING DATE: 1999-06-08
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Dumas Milne Edwards, J.B.
                                                                                                                                                                                                                                                                           LENGTH: 404
TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       OTHER INFORMATION: n = A,T,C or
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ORGANISM: Homo sapiens
FEATURE:
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                                                                                                                                                                                       Local Similarity
mes 37; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local
INFORMATION:
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                                                                                                                      348 GAGGAAGAAGGTGGGGAGGAAGAAGAAGAAGAATGTGA 391
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                                                                                                                                                                                         Conservative
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                                                                                                                                                                                                       64.3%;
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; Pred. No. 0.34
0; Mismatches
                                                                                                                                                                                       Score 32.8; DB 4; Pred. No. 0.37; 0; Mismatches 7;
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CURRENT APPLICATION NUMBER: US/09/620,312D
CURRENT FILING DATE: 2000-07-19
PRIOR APPLICATION NUMBER: 09/552,317
PRIOR FILING DATE: 2000-04-25
PRIOR APPLICATION NUMBER: 09/488,725
PRIOR FILING DATE: 2000-01-21
NUMBER OF SEQ ID NOS: 1105
SOFTWARE: pt_FL_genes Version 1.0
SEQ ID NO 1085
LENGTH: 2817
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (109)..(2817)
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                                                                                             Query Match
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CURRENT FILING DATE: 2001-06-28
NUMBER OF SEQ ID NOS: 64
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best Local Similarity 89. Matches 35; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Patent No.
                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Drmanac, Radoje T.
TITLE OF INVENTION: No. 6569662el Nucleic Acids and
TITLE OF INVENTION: Polypeptides
FILE REFERENCE: 784CIP2B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LENGTH: 661
TYPE: DNA
ORGANISM: HSV-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE DIAGNOSIS AND TITLE OF INVENTION: TREATMENT OF HERPES SIMPLEX VIRUS INFECTION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILE REFERENCE: 210121.538
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                                                                                Local
       209
                      l Similarity
37; Conserv
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Zhang, Jie
Ren, Feiyan
Chen, Rui-hong
Zhao, Qing A
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Xue, Aidong J.
                                                                                                                                                                                                                                                                                                                                                                                                                         Wang, Dunrui
Wang, Zhiwei
John Tillinghast
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Liu, Chenghua
                                                               Conservative
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Jian-Rui
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                                                                        63.1%;
82.2%;
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89.7%;
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                                                         Score 32.2; DB 4;
Pred. No. 0.65;
0; Mismatches 8;
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Pred. No. 0.44;
0; Mismatches 4;
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                                                                                     Length 2817;
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                                                         Indels
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RESULT 12
US-09-736-457-1668
^^~mence 1668, Application US/09736457
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; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-702-705-1668
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                                                                                                                                                                                   Query Match
Best Local Similarity
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SEQ ID NO 1668
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Matches
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SOFTWARE: FASESEQ for Windows Version 3.0
SEQ ID NO 1
LENGTH: 14561
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
APPLICANT: Scanlan, Matthew J.
APPLICANT: Gure, Ali O.
APPLICANT: Williamson, Barbara
APPLICANT: Chen, Yao-Tseng
APPLICANT: Old, Lloyd J.
TITLE OF INVENTION: Cancer Associated Antigens
TITLE OF INVENTION: Therefor
FILE REFERENCE: L0461/7062
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                CURRENT APPLICATION NUMBER: US/09/702,705
CURRENT FILING DATE: 2000-10-30
NUMBER OF SEQ ID NOS: 1833
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Mannion, Jane
APPLICANT: Fan, Liqun
TITLE OF INVENTION: COMPOSITIONS AND METHODS
TITLE OF INVENTION: DIAGNOSIS OF LUNG CANCER
FILE REFERENCE: 210121.478C14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Patent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CURRENT APPLICATION NUMBER: US/09/392,714A
CURRENT FILING DATE: 1999-09-09
EARLIER APPLICATION NUMBER: PCT/US98/14679
EARLIER FILING DATE: 1998-07-15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    6252 GAGGAGGAAGATGAGGAGGAGGAGGAAGAAGAGAGTGAA 6296
                                                                                                        586
                                                                                                                                                                       39;
                                                                                                                            1 GAGGATGAAGCTGAAGAGGAGGAGGAGGAGGAGGAGGAGGAGTGTGAACCCCAG 51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 GAGGATGAAGCTGAAGAGGAGGAGGAGGAGGAGGAGAGAGTGTGAA 45
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37; Conser
                                                                                               GAGGAGGAAGAAGAGGAGGAGGAGGAGGATGAATAATGACTCGAG 636
                                                                                                                                                                                                                                                                                                                FastSEQ for Windows Version 3.0
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Vedvick, Tom
Carter, Darrick
Retter, Marc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bangur, Chaitanya
Lodes, Michael A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Wang,
                                                                                                                                                                      Conservative
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82.2%;
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INFORMATION:

Bangur, Chaitanya Lodes, Michael A.

Tongtong r, Chaitanya

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RESULT 14
US-09-671-325-1668
; Sequence 1668, Application US/09671325
; Patent No. 6667154
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; Sequence 1668, Application US/09614124B
; Patent No. 6630574
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SEQ ID NO 1668
LENGTH: 636
                                                                                                                                                                                                                                                                             SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 1668
LENGTH: 636
TYPE: DNA
                                                                                                                                                                            Matches
                                                                                                                                                                                                        Query Match
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ORGANISM: Homo sapiens
-09-736-457-1668
                                                                                                                                                                                                                                                                                                                                          APPLICANT: Mannion, Jane
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THERAPY AND
TITLE OF INVENTION: DIAGNOSIS OF LUNG CANCER
FILE REFERENCE: 210121.478C9
CURRENT APPLICATION NUMBER: US/09/614,124B
CURRENT FILING DATE: 2001-07-11
NUMBER OF SEQ ID NOS: 1668
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Wang, Tongtong
APPLICANT: Bangur, Chaitanya
APPLICANT: Lodes, Michael A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CURRENT APPLICATION NUMBER: US/09/736,457
CURRENT FILING DATE: 2000-12-13
NUMBER OF SEQ ID NOS: 1864
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Wang, Aijun
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
TITLE OF INVENTION: DIAGNOSIS OF LUNG CANCER
FILE REFERENCE: 210121.478C15
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                                                                                                        985
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                                                                                                                                      1 GAGGATGAAGCTGAAGAGGAGGAGGAGGAGGAGGAGGAGGAGTGTGAACCCCCAG 51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 GAGGATGAAGCTGAAGAGGAGGAGGAGGAGGAGGAGTGTGAACCCCCAG 51
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Carter, Darrick
Retter, Marc
                                                                                                      GAGGAGGAAGAAGAGGAGGAGGAGGAGGATGAATAATGACTCGAG 636
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Mannion, Jane
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Vedvick, Tom
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Pred. No. 0.74;
0; Mismatches
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Pred. No. 0.74;
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; ORGANISM: Homo sapiens
US-09-671-325-1668
  Search completed: March
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; SEQ ID NO 1668
; LENGTH: 636
                                                                                                                                    Matches
                                                                                                                                                    Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                        SEQ ID NO 21
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Patent No. 6399373
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Best Local Similarity
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TITLE OF INVENTION: A NUCLEIC ACID ENCODING A RETINOBLASTOMA BINDING PROTEIN (RBP-7)
TITLE OF INVENTION: AND POLYMORPHIC MARKERS ASSOCIATED WITH SAID NUCLEIC ACID.
FILE REFERENCE: GENSET.031A
CURRENT APPLICATION NUMBER: US/09/345,882
CURRENT FILING DATE: 1999-06-30
PRIOR APPLICATION NUMBER: US 60/091,315
PRIOR FILING DATE: 1998-06-30
PRIOR APPLICATION NUMBER: US 60/111,909
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Fan, Liqun
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
TITLE OF INVENTION: DIAGNOSIS OF LUNG CANCER
FILE REFERENCE: 210121.478C12
CURRENT APPLICATION NUMBER: US/09/671,325
CURRENT FILLING DATE: 2000-09-26
CURRENT FILLING DATE: 2000-09-26
CURRENT FILLING DATE: 2000-09-26
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                                                                                                                                                                                                                                                                                                          SOFTWARE: Patent.pm
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                                                                                                                                                                                                                            TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                    LENGTH: 258
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                                                          32 GATGAAGAAGCAGAAGAGGAGGAGGAGGAAGAAGA 69
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Vedvick, Tom
Carter, Darrick
Retter, Marc
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Lodes, Michael
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Pred. No. 0.74;
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Minimum DB
Maximum DB
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Maximum Match 100%
Listing first 45 s
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1: /cgn2_6/ptodata/2/pubpna/US07 PUBCOMB.seq:*

2: /cgn2_6/ptodata/2/pubpna/PCT_NEW PUB.seq:*

3: /cgn2_6/ptodata/2/pubpna/US06_NEW PUB.seq:*

4: /cgn2_6/ptodata/2/pubpna/US06_PUBCOMB.seq:*

5: /cgn2_6/ptodata/2/pubpna/US07_NEW PUB.seq:*

6: /cgn2_6/ptodata/2/pubpna/US08_NEW PUB.seq:*

6: /cgn2_6/ptodata/2/pubpna/US08_NEW PUB.seq:*

7: /cgn2_6/ptodata/2/pubpna/US08_PUBCOMB.seq:*

9: /cgn2_6/ptodata/2/pubpna/US09A_PUBCOMB.seq:*

10: /cgn2_6/ptodata/2/pubpna/US09A_PUBCOMB.seq:*

11: /cgn2_6/ptodata/2/pubpna/US09C_PUBCOMB.seq:*

12: /cgn2_6/ptodata/2/pubpna/US09C_PUBCOMB.seq:*

13: /cgn2_6/ptodata/2/pubpna/US09C_PUBCOMB.seq:*

14: /cgn2_6/ptodata/2/pubpna/US09C_PUBCOMB.seq:*

16: /cgn2_6/ptodata/2/pubpna/US09C_PUBCOMB.seq:*

16: /cgn2_6/ptodata/2/pubpna/US10A_PUBCOMB.seq:*

16: /cgn2_6/ptodata/2/pubpna/US10C_PUBCOMB.seq:*

17: /cgn2_6/ptodata/2/pubpna/US10C_PUBCOMB.seq:*

18: /cgn2_6/ptodata/2/pubpna/US10_NEW_PUB.seq:*

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10: /cgn2_6/ptodata/2/pubpna/US10_NEW_PUB.seq:*

10: /cgn2_6/ptodata/2/pubpna/US10_NEW_PUB.seq:*
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length: 2000000000
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Match
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   14 US-10-311-455-47
10S-09-825-923-3
4 US-10-077-870-3
4 US-10-007-870-3
15 US-10-305-720-1181
4 US-10-225-567A-41
4 US-10-128-714-7204
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US-09-825-923-1
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Sequence 2, Appli
Sequence 1, Appli
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Sequence 41, Appli
Sequence 6204, App
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US-09-825-923-1
J Sequence 1, Application US/09825923
J Patent NO. US20010016338A1
J GENERAL INFORMATION:
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US-10-001-073-2
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             APPLICANT: Snapir, Amir
APPLICANT: Heinonen, Paula
APPLICANT: Alhopuro, Pia
APPLICANT: Karyonen, Matti
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US-09-879-536-33 US-10-424-599-60174 US-10-029-386-18468 US-09-728-444-146 US-09-728-445-59 US-09-728-045-59 US-10-085-117-303 US-10-085-117-303 US-10-027-632-13656 US-10-027-632-1325232 US-10-027-632-325232 US-10-029-386-4792 US-10-029-386-24791 US-10-029-386-24791 US-10-320-797-316 US-10-320-797-316 US-10-320-797-316 11 US-09-864-408A-3111 15 US-10-191-803-61 19 US-09-844-864-5 19 US-09-844-864-5 19 US-10-424-599-108927 10 US-10-369-493-27799 10 US-10-205-194-145 10 US-10-205-194-145 10 US-09-864-761-23094 US-09-918-995-27029 US-09-864-761-6378 US-10-242-535A-43536 Sequence 3111, Ap Sequence 11, Appli Sequence 12, Appli Sequence 109927, Sequence 27999, Sequence 27999, Sequence 27029, Sequence 27029, Sequence 31336, Appli Sequence 6378, Appli Sequence 6378, Appli Sequence 10174, Appli Sequence 19468, Appli Sequence 19455, Appli Sequence 194255, Sequence 375232, Sequence 375232, Sequence 375232, Sequence 375232, Sequence 375232, Sequence 194255, Sequence 375232, Sequence 194255, Sequence 375232, Sequence 194255, Sequence 194255, Sequence 375232, Sequence 1194255, Sequence 1194255,

## ALIGNMENTS

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APPLICANT: Liggett, Stephen
APPLICANT: Small, Kirsten
TITLE OF INVENTION: Alpha-2-adrenergic receptor polymorphisms
FILE REPERENCE: 13073-PCT
CURRENT APPLICATION NUMBER: US/10/001,073
CURRENT FILING DATE: 2001-11-01
NUMBER OF SEQ ID NOS: 53
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 2
LENGTH: 1344
TYPE: DNA
ORGANISM: Homo sapiens
US-10-001-073-2
                                                                                           Query Match 100.0%; Score 51; DB 14; Best Local Similarity 100.0%; Pred. No. 9.9e-07; Matches 51; Conservative 0; Mismatches 0;
                          1 GAGGATGAAGCTGAAGAGGAGGAGGAGGAGGAGGAGAGTGTGAACCCCAG
GAGGATGAAGCTGAAGAGGAGGAGGAGGAGGAGGAAGAGTGTGAACCCCAG 930
                                                                                                                                                Length 1344;
                                                                                                   Indels
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                                                                                                Gaps
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Result

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RESULT 4
US-10-311-455-47
                                                                                                                                                                                                          ; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(1341)
; OTHER INFORMATION: Coding sequence for variant human alpha-2B-adrenoceptor protein US-10-077-870-1
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                                                                                                                                                                              Query Match
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SOFTWARE: PatentIn Ver. 3.1
SEQ ID NO 1
LENGTH: 1344
                                                                                                                                            Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 1, Application US/10077870 Publication No: US20030003470A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Salonen, Jukka T
TITLE OF INVENTION: Method for detecting a risk of hypertension and uses thereof
FILE REFERENCE: 0933-01839
CURRENT APPLICATION NUMBER: US/10/077,870
CURRENT FILING DATE: 2002-05-21
PRIOR APPLICATION NUMBER: FI 20010323
PRIOR PETING DATE: 2001-02-20
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Best Local Similarity
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SEQ ID NO 1
                                                                                                                                                                                                                                                                                                                        TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Kauhanen, Jussi
APPLICANT: Valkonen, Veli-Pekka
TITLE OF INVENTION: A DNA molecule encoding a variant alpha-2B-adrenoceptor
TITLE OF INVENTION: Protein, and uses thereof
FILE REFERENCE: Alpha-2B-AR variant
CURRENT APPLICATION NUMBER: US/09/825,923
EUROB APPLICATION NUMBER: US/09/825,923
EUROB APPLICATION UND APPLICATION NUMBER: US/09/825,923
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CURRENT FILING DATE: 2001-04-05
PRIOR APPLICATION NUMBER: 09/422,985
PRIOR FILING DATE: 2000-05-25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME/KEY: CDS
LOCATION: (1)...(1341)
COTHER INFORMATION: Coding sequence for variant human
OTHER INFORMATION: alpha-2B-adrenoceptor protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: DNA
ORGANISM: Homo sapiens
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                                                                                                                                                           Local Similarity
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                                                                             1 GAGGATGAAGCTGAAGAGGAGGAGGAGGAGGAGGAAGAGTGTGAACCCCAG 51
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                                                      GAGGATGAAGCTGAAGAGGAGGAAGAGGAGGAGGAGTGTGAACCCCCAG 930
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Salonen, Riitta
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Salonen, Jukka T
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                                                                                                                                                   93.7%;
96.1%;
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96.1%;
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                                                                                                                             Score 47.8; DB 14;
Pred. No. 9.5e-06;
0; Mismatches 2;
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Pred. No. 9.5e-06;
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                                                                                                                                                               Length 1344;
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                                                                   SEQ ID NO 3
                                                                                                                              APPLICANT: Lakka, Timo A
APPLICANT: Lakka, Timo A
APPLICANT: Salonen, Kristiina
APPLICANT: Salonen, Riitta
APPLICANT: Kauhanen, Jussi
APPLICANT: Kauhanen, Jussi
APPLICANT: Valkonen, Veli-Pekka
TITLE OF INVENTION: A DNA molecule encoding a variant alpha-2B-adrenoceptor
FILE REFERENCE: Alpha-2B-AR variant
CURRENT FILING DATE: 2001-04-05
CURRENT FILING DATE: 2001-04-05
CURRENT FILING DATE: 2001-04-05
CURRENT FILING DATE: 2001-04-05
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APPLICANT: BERLIN, Kurt
TITLE OF INVENTION: Diagnosis of Diseases Associated with the Immune System by Determ;
FILE REFERENCE: 5013.1014
CURRENT APPLICATION NUMBER: US/10/311,455
CURRENT FILING DATE: 2002-12-16
PRIOR APPLICATION NUMBER: PCT/EP01/07537
PRIOR APPLICATION NUMBER: DC 10032529.7
PRIOR APPLICATION NUMBER: DE 10032529.7
PRIOR APPLICATION NUMBER: DE 10043826.1
NUMBER OF SEQ ID NOS: 2424
LENGTH. 6004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence
                                                                                                   NUMBER OF SEQ ID NOS:
                                                                                                                    PRIOR APPLICATION NUMBER: 09/422,985
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Patent No. US20010016338A1
                                 LENGTH: 1353
TYPE: DNA
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Best Local
ORGANISM: Homo sapiens FEATURE:
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Publication No. US20030143606A1
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NAME/KEY: unsure
LOCATION: 6084
OTHER INFORMATION: n is a or g or
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OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: OLEK, Alexander APPLICANT: PIEPENBROCK, C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH: 6904
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                                                                                PatentIn Ver. 2.1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        43;
                                                                                                                                                                                                                                                                                                                          Pesonen, Ullamari
Scheinin, Mika
Salonen, Jukka T
Tuomainen, Tomi-Pekka
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Similarity 95.6
43; Conservative
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Koulu, Markku
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Alhopuro, Pia
                                                                                                   2000-05-25
)S: 10
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Pred. No. 0
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.00064;
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US-10-001-073-1
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                                                                                                                                              JS-10-001-073-1
                                                                      Matches
                                                                                                        Query Match
                                                                                                                                                                                                                    SEQ ID NO 1
                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
                                                                                                                                                                                                                                                                    APPLICANT: Liggett, Stephen
APPLICANT: Small, Kirsten
TITLE OF INVENTION: Alpha-2-adrenergic receptor polymorphisms
FILE REFERENCE: 13073-PCT
CURRENT APPLICATION NUMBER: US/10/001,073
CURRENT FILING DATE: 2001-11-01
                                                                                                                                                                                                                                 NUMBER OF SEQ ID NOS: 53
SOFTWARE: PatentIn Ver.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION NUMBER: FI 20010323
PRIOR FILING DATE: 2001-02-20
NUMBER OF SEQ ID NOS: 10
SOFTWARE: Patentin Ver. 3.1
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TITLE OF INVENTION: Method for detecting a
FILE REFERIOE: 0933-0183P
CURRENT APPLICATION NUMBER: US/10/077,870
CURRENT FILING DATE: 2002-05-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FEATURE:
NAME/KEY: CDS
LOCATION: (1)..(1350)
OTHER INFORMATION: Coding sequence for human alpha-2B-adrenoceptor protein
                                                                                                                                                         LENGTH: 1353
TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LENGTH: 1353
TYPE: DNA
ORGANISM: Homo sapiens
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OTHER INFORMATION: Coding sequence for human alpha-2B-adrenoceptor
OTHER INFORMATION: protein
                                                                                         Local Similarity
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                                                                    44; Conservative
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                                GATGAAGCTGAAGAGGAGGAGGAGGAGGAAGAGTGTGAACCCCAG 51
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91.7%;
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91.7%;
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91.7%;
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                                                                                     Score 41.6; DB 14
Pred. No. 0.00075;
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Pred. No. 0.00075;
                                                                      Mismatches
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RESULT 10
US-10-128-714-6204
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                                                                                                                                                                                                                                                                                                                                               SOFTWARE: PatentIn version 3.1
SEQ ID NO 41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 1181, Application US/10305720 Publication No. US20040010136A1 GENERAL INFORMATION:
                                                                                                                                                                                                  Query Match
Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 41, Application US/10225567A Publication No. US20030113798A1
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                                                                                                                                                                                                                                                                                                                                                                                          TITLE OF INVENTION: ANTIGENIC PERTIDES AND ANTIBODIES FOR G PROTEIN-COUPLED RECEPTORS FILE REFERENCE: 1920-4-4 CURRENT APPLICATION NUMBER: US/10/225,567A CURRENT FILING DATE: 2001-12-19 PRIOR APPLICATION NUMBER: 60/257,144 PRIOR APPLICATION NUMBER: 60/257,144 PRIOR FILING DATE: 2000-12-19 NUMBER OF SEQ ID NOS: 2292
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Au-Young, Janice K.; Seilhamer, Jeffrey J.
TITLE OF INVENTION: Composition for the Detection of Signaling Pathway Gene Expression FILE REFERENCE: PA-0002-1 CON
CURRENT APPLICATION NUMBER: US/10/305,720
CURRENT FILING DATE: 2002-11-26
PRIOR APPLICATION NUMBER: 09/016,434
PRIOR APPLICATION NUMBER: 09/016,434
PRIOR FILING DATE: 1998-01-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT:
                                                                                                                                                                                                                                                                                  TYPE: DNA ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: LifeSpan Biosciences
                                                                                                                                                                                                                                                                                                          LENGTH: 3274
TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ORGANISM: Homo sapiens FEATURE: NAME/KEY: misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           OTHER INFORMATION: GenBank ID No. US20040010136A1 g178197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: DNA
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                                                                                                                                                                         Local Similarity
les 44; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1304 GAAGAGGAGGAGGAGGAGGAGGAGGAGGAGTGTGAACCCCCAG
                                                                                        892 GAAGAGGAAGAAGAGGAGGAGGAGGAAGAAGAGTGTGAACCCCCAG
                                                                                                                                 4 GATGAAGCTGAAGAGGAGGAGGAGGAGGAAGAGTGTGAACCCCCAG
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Burmer, Glenna C.
Roush, Christine L.
                                                                                                                                                                            Conservative
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                                                                                                                                                                         Score 41.6; DB 14;
Pred. No. 0.00074;
0; Mismatches 4;
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Pred. No. 0.00074;
0; Mismatches 4;
                                                                                                                                                                                                                    Length 3274;
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APPLICANT: Jiang, B

Во

Sequence 6204, Application US/10128714 Publication No. US20030119013A1

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APPLICANT: Lemieux, Sebastien M
TITLE OF INVENTION: Identification of Essential Genes in Aspergillus fumigatus and
TITLE OF INVENTION: Identification of Essential Genes in Aspergillus fumigatus and
FILTE REFERENCE: 10182-018-999
CURRENT APPLICATION NUMBER: US/10/128,714
PRIOR APPLICATION NUMBER: US/20/24-23
PRIOR APPLICATION NUMBER: US 60/285,697
PRIOR FILING DATE: 2001-04-23
PRIOR FILING DATE: 2001-04-23
PRIOR APPLICATION NUMBER: US 60/287,066
PRIOR APPLICATION NUMBER: US 60/295,890
PRIOR APPLICATION NUMBER: US 60/295,890
PRIOR APPLICATION NUMBER: US 60/303,899
PRIOR FILING DATE: 2001-07-09
PRIOR FILING DATE: 2001-07-09
PRIOR FILING DATE: 2001-08-31
NUMBER OF SEO ID NOS: 4601
                                                                                                      ORGANISM: Aspergillus
US-10-128-714-7204
                                                                                                                                   SOFTWARE: PatentIn version 3.1
SEQ ID NO 7204
LENCTH: 2367
TYPE: DNA
                                  Matches
                                                                 Query Match
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US-10-128-714-6204
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PRIOR APPLICATION NUMBER: US 60/285,697
PRIOR FILING DATE: 2001-04-23
PRIOR PRICATION NUMBER: US 60/287,066
PRIOR APPLICATION NUMBER: US 60/287,066
PRIOR FILING DATE: 2001-04-27
PRIOR APPLICATION NUMBER: US 60/295,890
PRIOR FILING DATE: 2001-06-05
PRIOR FILING DATE: 2001-06-05
PRIOR FILING DATE: 2001-06-05
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 7204, Application US/10128714 Publication No. US20030119013A1
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LENGTH: 2367
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PRIOR FILING DATE: 2001-07-09
PRIOR APPLICATION NUMBER: US 60/316,362
PRIOR FILING DATE: 2001-08-31
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APPLICANT: Lemieux, Sebastien M
TITLE OF INVENTION: Identification of Essential Genes in Aspergillus fumigatus and
FILE REFERENCE: 10.182-018-999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: DNA
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                     1 Similarity 88.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            39;
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Tishkoff, Daniel
Zamudio, Carlos
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Zamudio, Carlos
                                      70.6%;
                                                                                                                fumigatus
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          Score 36; DB:
Pred. No. 0.031
0; Mismatches
                     0
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Pred. No. 0.038;
0; Mismatches
                               DB 14; Length 2367;
).038;
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APPLICANT: Hu, Wenqi
APPLICANT: Hu, Wenqi
APPLICANT: Hu, Wenqi
APPLICANT: Tishkoff, Daniel
APPLICANT: Zamudio, Carlos
APPLICANT: Zamudio, Carlos
APPLICANT: Eroshkin, Alexey M
TITLE OF INVENTION: Methods of Use
TITLE OF INVENTION: Methods of Use
CURRENT APPLICATION NUMBER: US/10/128,714
PRIOR APPLICATION NUMBER: US 60/285,697
PRIOR APPLICATION NUMBER: US 60/287,066
PRIOR APPLICATION NUMBER: US 60/287,066
PRIOR FILLING DATE: 2001-04-23
PRIOR FILLING DATE: 2001-04-27
PRIOR APPLICATION NUMBER: US 60/287,066
PRIOR APPLICATION NUMBER: US 60/287,066
PRIOR APPLICATION NUMBER: US 60/287,066
PRIOR FILLING DATE: 2001-04-27
PRIOR FILLING DATE: 2001-04-27
PRIOR APPLICATION NUMBER: US 60/295,890
PRIOR APPLICATION NUMBER: US 60/205,890
PRIOR FILLING DATE: 2001-07-09
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APPLICANT: Lemieux, Sebastien M
TITLE OF INVENTION: Identification of Essential Genes in Aspergillus fumigatus and
ITILE OF INVENTION: Methods of Use
CURRENT SEFERENCE: 10182-018-999
CURRENT APPLICATION NUMBER: US/10/128,714
PRIOR APPLICATION NUMBER: US 60/285,697
PRIOR APPLICATION NUMBER: US 60/285,890
PRIOR FILING DATE: 2001-04-27
PRIOR APPLICATION NUMBER: US 60/295,890
PRIOR FILING DATE: 2001-06-05
PRIOR FILING DATE: 2001-08-05
PRIOR APPLICATION NUMBER: US 60/303,899
PRIOR APPLICATION NUMBE
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; ORGANISM: Aspergillus fumigatus
US-10-128-714-204
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LENGTH: 4238
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US-10-128-714-204
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APPLICANT: Hu, Wengi
APPLICANT: Tishkoff, Daniel
APPLICANT: Zamudio, Carlos
APPLICANT: Zamudio, Tarios
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 GAGGATGAAGCTGAAGAGGAGGAGGAGGAGGAGGAGAGAGTGTGA 44
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o. US20030119013A1
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Pred. No. 0.
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; PRIOR APPLICATION NUMBER: US 60/316,362
; PRIOR FILING DATE: 2001-08-31
; NUMBER OF SEQ ID NOS: 8603
; SOPTWARE: PatentIn version 3.1
; SEQ ID NO 5204
; LENGTH: 4367
; TYPE: DNA
; ORGANISM: Aspergillus fumigatus
US-10-128-714-5204
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US-10-424-599-94653
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US-10-424-599-139707
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US-10-424-599-139707
                                                                                                                                                                                                                                                                                                                                                                                         Sequence 94653, Application US/10424599
Publication No. US20040031072A1
GENERAL INFORMATION:
APPLICANT: La Rosa Thomas J
APPLICANT: Kovalic David K
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQ ID NOS: 285684
SEQ ID NO 139707
LENGTH: 1012
                                                                                                                              NUMBER OF SEQ ID NOS: 285684
SEQ ID NO 94653
LENGTH: 1554
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Zhou Yihua
APPLICANT: Cao Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(5323)B
CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT FILING DATE: 2003-04-28
                                                                                                                                                                                                         APPLICANT: Zhou Yihua
APPLICANT: Cao Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(53223)8
FULE REFERENCE: 38-21(53223)8
CURRENT PPLICATION NUMBER: US/10/424,599
CURRENT FILING DATE: 2003-04-28
OTHER INFORMATION: Clone ID: PAT_MRT3847_56483C.1 10-424-599-94653
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ORGANISM: Glycine max FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: La Rosa Thomas J
                                                                                                        TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: DNA
                                                                             ORGANISM: Glycine max
                                                       FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            / Match 69.8%; Score 35.6; DB 12; Length 1012; Local Similarity 82.0%; Pred. No. 0.051; ndels 0; 41; Conservative 0; Mismatches 9; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3314 GAGGAGGAAGAAGAAGAGGAGGAAGAAGAAGAGTTTGA 3357
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      467 GAAGAAGACGTAGAAGAGGAGGAGGAGGAGGAGAGTTTGAAGACGA 516
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 GAGGATGAAGCTGAAGAGGAGGAGGAGGAAGAGTGTGAACCCCA 50
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Search completed: March Job time : 141 secs

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45: /cgm2 6/ picodata // jpma //ISS 101A COMB. seq: 48: /cgm2 6/ picodata // jpma //ISS 101A COMB. seq: 48: /cgm2 6/ picodata // jpma //ISS 102A COMB. seq: 49: /cgm2 6/ picodata // jpma //ISS 102A COMB. seq: 50: /cgm2 6/ picodata // jpma //ISS 103A COMB. seq: 50: /cgm2 6/ picodata // jpma //ISS 103A COMB. seq: 50: /cgm2 6/ picodata // jpma //ISS 103A COMB. seq: 50: /cgm2 6/ picodata // jpma //ISS 103A COMB. seq: 50: /cgm2 6/ picodata // jpma //ISS 103A COMB. seq: 50: /cgm2 6/ picodata // jpma //ISS 103A COMB. seq: 50: /cgm2 6/ picodata // jpma //ISS 103A COMB. seq: 50: /cgm2 6/ picodata // jpma //ISS 103A COMB. seq: 50: /cgm2 6/ picodata // jpma //ISS 103A COMB. seq: 50: /cgm2 6/ picodata // jpma //ISS 103A COMB. seq: 50: /cgm2 6/ picodata // jpma //ISS 103A COMB. seq: 50: /cgm2 6/ picodata // jpma //ISS 103A COMB. seq: 50: /cgm2 6/ picodata // jpma //ISS 103A COMB. seq: 50: /cgm2 6/ picodata // jpma //ISS 103A COMB. seq: 50: /cgm2 6/ picodata // jpma //ISS 103A COMB. seq: 50: /cgm2 6/ picodata // jpma //ISS 103A COMB. seq: 50: /cgm2 6/ picodata // jpma //ISS 103A COMB. seq: 50: /cgm2 6/ picodata // jpma //ISS 103A COMB. seq: 50: /cgm2 6/ picodata // jpma //ISS 103A COMB. seq: 50: /cgm2 6/ picodata // jpma //ISS 103A COMB. seq: 50: /cgm2 6/ picodata // jpma //ISS 103A COMB. seq: 50: /cgm2 6/ picodata // jpma //ISS 103A COMB. seq: 50: /cgm2 6/ picodata // jpma //ISS 103A COMB. seq: 50: /cgm2 6/ picodata // jpma //ISS 103A COMB. seq: 50: /cgm2 6/ picodata // jpma //ISS 103A COMB. seq: 50: /cgm2 6/ picodata // jpma //ISS 103A COMB. seq: 50: /cgm2 6/ picodata // jpma //ISS 103A COMB. seq: 50: /cgm2 6/ picodata // jpma //ISS 103A COMB. seq: 50: /cgm2 6/ picodata // jpma //ISS 103A COMB. seq: 50: /cgm2 6/ picodata // jpma //ISS 103A COMB. seq: 50: /cgm2 6/ picodata // jpma //ISS 103A COMB. seq: 50: /cgm2 6/ picodata // jpma //ISS 103A COMB. seq: 50: /cgm2 6/ picodata // jpma //ISS 103A COMB. seq: 50: /cgm2 6/ picodata // jpma //ISS 103A COMB. seq: 50: /cgm2 6/ picodata // jpma //ISS 103A COMB. seq: 50: /cgm2 6/ picod
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Result No.

% Query Match Length DB

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500

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US-09-949-004-175
US-10-305-720-1181
US-10-225-567A-41
7 US-60-500-315-890
7 US-60-500-315-891
US-60-207-360-68
US-60-207-360-111
US-60-207-360-111
US-60-207-360-112
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US-60-159-840-3708
US-60-159-841-172
US-60-159-847-3351
US-60-159-847-3351
US-09-492-0778-1
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US-09-692-0778-1
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US-09-692-0778-1
US-09-692-0773-1
US-10-001-073-1
US-10-001-073-1
US-10-01-073-1
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US-09-825-923-1
US-10-077-870-1
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US-60-160-189-1492
US-60-160-190-231
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US-60-169-842-1935
US-60-170-346-61
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US-60-468-720-1259
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Sequence 2, Appli

Sequence 2, Appli

Sequence 2, Appli

Sequence 25, Appli

Sequence 1, Appli

Sequence 1, Appli

Sequence 1, Appli

Sequence 1935, Appli

Sequence 1935, Appli

Sequence 1935, Appli

Sequence 1492, Appli

Sequence 231, Appli

Sequence 231, Appli

Sequence 2172, Appli

Sequence 1172, Appli

Sequence 1172, Appli

Sequence 1, Appli

Sequence 3, Appli

Sequence 407119, Appli

Sequence 6437, Appli
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Sequence 4067, Ap
Sequence 1259, Ap
APPLICANT: CASTLE, Arthur
APPLICANT: Castle, Arthur
APPLICANT: Castle, Arthur
APPLICANT: Elashoff, Michael
APPLICANT: Gene Logic, Inc.
TITLE OF INVENTION: Molecular Hepatotoxicology Modeling
FILE REFERENCE: 44921-5038-P15
CURRENT APPLICATION NUMBER: US 60/222,040
PRIOR APPLICATION NUMBER: US 60/222,040
PRIOR APPLICATION NUMBER: US 60/222,040
PRIOR APPLICATION NUMBER: US 60/290,029
PRIOR APPLICATION NUMBER: US 60/290,029
PRIOR FILING DATE: 2001-05-11
PRIOR APPLICATION NUMBER: US 60/290,645
PRIOR APPLICATION NUMBER: US 60/290,645
PRIOR APPLICATION NUMBER: US 60/292,336
PRIOR PILING DATE: 2001-05-15
PRIOR PILING DATE: 2001-05-22
PRIOR PILING DATE: 2001-05-25
PRIOR APPLICATION NUMBER: US 60/295,798
PRIOR APPLICATION NUMBER: US 60/297,457
PRIOR FILING DATE: 2001-06-13
PRIOR FILING DATE: 2001-06-13
PRIOR APPLICATION NUMBER: US 60/298,884
PRIOR FILING DATE: 2001-06-13
PRIOR APPLICATION NUMBER: US 60/303,459
PRIOR APPLICATION NUMBER: US 60/303,459
PRIOR FILING DATE: 2001-07-09
PRIOR APPLICATION NUMBER: US 60/303,459
PRIOR FILING DATE: 2001-07-09
PRIOR APPLICATION NUMBER: US 60/303,459
PRIOR APPLICATION NUMBER: US 60/303,459
PRIOR FILING DATE: 2001-07-09
PRIOR 
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US-60-436-643-4067
October 4067, Ap
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; OTHER INFORMATION: Genbank Accession No. S67316
PCT-US03-03194-4067
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GENERAL I
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PRIOR APPLICATION NUMBER: US 60/290,645
PRIOR FILING DATE: 2001-05-15
PRIOR APPLICATION NUMBER: US 60/292,336
PRIOR APPLICATION NUMBER: US 60/295,798
PRIOR APPLICATION NUMBER: US 60/295,798
PRIOR FILING DATE: 2001-06-06
PRIOR PILING DATE: 2001-06-06
PRIOR APPLICATION NUMBER: US 60/297,457
PRIOR FILING DATE: 2001-06-13
PRIOR APPLICATION NUMBER: US 60/298,884
PRIOR FILING DATE: 2001-06-19
PRIOR APPLICATION NUMBER: US 60/303,459
PRIOR PILING DATE: 2001-07-09
PRIOR APPLICATION NUMBER: US 60/331,273
PRIOR PILING DATE: 2001-11-13
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SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 4067
LENGTH: 828
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Best Local !
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APPLICANT: Porter, Mark
APPLICANT: Johnson, Kory
APPLICANT: Castle, Arthur
APPLICANT: Clastle, Michael
APPLICANT: Elashoff, Michael
APPLICANT: Gene Trois Tipel
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       595 GAGGATGAAGCTGAAGAGGAGGAGGAGGAAGAGTGTGAACCCCCAG 645
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Pred. No. 0.019;
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47.8 47.8 47.8 41.8 41.6

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PCT-USO3-03194-4067

Sequence 4067, Application PC/TUS0303194

GENERAL INFORMATION:

APPLICANT: Mendrick, Donna
APPLICANT: Johnson, Kory
APPLICANT: Johnson, Kory
APPLICANT: Gastle, Arthur
APPLICANT: Gastle, Arthur
APPLICANT: Gastle, Arthur
APPLICANT: Glashoff, Michael
APPLICANT: Blashoff, Michael
APPLICANT: Blashoff, Michael
APPLICANT: Blashoff, Michael
APPLICANT: Brishoff, Michael
APPLICANT: Brishoff, Michael
APPLICANT: Brishoff, Michael
APPLICANT: Blashoff, Michael
APPLICANT: Molecular Hepatotoxicology Modeling
FILE REFERENCE: 44921-5038-01-W0

CURRENT APPLICATION NUMBER: ECT/US03/03194

CURRENT FILING DATE: 2003-01-31

PRIOR APPLICATION NUMBER: US 60/222,040

PRIOR FILING DATE: 2000-07-31

PRIOR APPLICATION NUMBER: US 60/222,880

PRIOR APPLICATION NUMBER: US 60/222,880

PRIOR APPLICATION NUMBER: US 60/290,029
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RESULT 4
US-09-692-077B-2
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US-60-468-720-1259
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-60-468-720-1259
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION NUMBER: US 60/396,145
PRIOR FILING DATE: 2003-05-06
PRIOR FILING DATE: 2002-07-17
NUMBER OF SEQ ID NOS: 1347
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 1259
LENGTH: 828
TYPE: Par
                                                                                                                      SEQ ID NO 2
LENGTH: 1344
TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                    Sequence 2, Application US/09692077B GENERAL INFORMATION:
                                                Query Match
Best Local Similarity
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                                   Matches
                                                                                                         ·09-692-077B-2
                                                                                                                                                                                                                               PILE REFERENCE: Sequences 1-22
CURRENT APPLICATION NUMBER: US/09/692,077B
CURRENT FILING DATE: 2000-10-19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILE REFERENCE: 44921-5124-P1
CURRENT APPLICATION NUMBER: US/60/468,720
CURRENT FILING DATE: 2003-05-06
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Higgs, Brandon APPLICANT: Castle, Arthu APPLICANT: Elashoff, Mic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH: 828
TYPE: DNA
                                                                                                                                                                                            SOFTWARE: Patentin Ver. 2.0
                                                                                                                                                                                                                                                                                 APPLICANT: Liggett, Stephen
TITLE OF INVENTION: Alpha-2B-adrenergic receptor polymorphisms
                                                                                                                                                                                                                NUMBER OF SEQ ID NOS: 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TITLE OF INVENTION: Nucleic Acid Detection
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ORGANISM: Rattus norvegicus FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: DNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         OTHER INFORMATION: Genbank Accession No. S67316
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Match 100.0%;
Local Similarity 100.0%;
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1 GAGGATGAAGCTGAAGAGGAGGAGGAGGAGGAGGAGTGTGAACCCCCAG
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Elashoff, Michael
Johnson, Kory
Porter, Mark
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ilarity 100.0%;
Conservative (
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                                   Conservative
                               100.0%; Score 51; DB 29;
100.0%; Pred. No. 0.019;
ative 0; Mismatches 0;
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Pred. No. 0.019;
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Pred. No. 0.019;
); Mismatches
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                                                                  Length 1344;
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US-10-001-073A-2
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; ORGANISM: Homo sapiens
US-09-692-077D-2
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                                                                                                                                                                                                                         Sequence 2, Application US/10001073A GENERAL INFORMATION:
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Best Local (
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                                    SOFTWARE: PatentIn version 3.2 SEQ ID NO 2
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APPLICANT: Small, Kirsten
TITLE OF INVENTION: Alpha-2-adrenergic receptor polymorphisms
FILE REFERENCE: 13073-PCT
CURRENT APPLICATION NUMBER: US/10/001,073
CURRENT FILLING DATE: 2001-11-01
NUMBER OF SEQ ID NOS: 53
                                                                         CURRENT APPLICATION NUMBER: US/10/001,073A
CURRENT FILING DATE: 2001-11-01
NUMBER OF SEQ ID NOS: 69
                                                                                                                                       APPLICANT: Small, Kersten M.
APPLICANT: Liggett, Stephen
TITLE OF INVENTION: Alpha-2 Adrenergic Receptor Polymorphisms
FILE REFERENCE: 10738-42
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APPLICANT: Small, Kersten M.
TITLE OF INVENTION: Alpha-2B-Adrenergic Receptor Polymorphisms
FILE REFERENCE: 10738-43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: DNA
ORGANISM: Homo sapiens
TYPE: DNA
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                     ENGTH: 1344
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Local Similarity 100.0%; Pred. No. 0.019;
nes 51; Conservative 0; Mismatches
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100.0%; Pred. No. 0.019;
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ORGANISM: Homo sapiens

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Sequence 25, Application US/09692077D
GENERAL INFORMATION:
APPLICANT: Liggett, Stephen
APPLICANT: Small, Kersten M.
TITLE OF INVENTION: Alpha-2B-Adrenergic Receptor Polymorphisms
FILE REFERENCE: 10738-43
CURRENT APPLICATION NUMBER: US/09/692,077D
CURRENT FILING DATE: 2000-10-19
NUMBER OF SEQ ID NOS: 26
SOFTWARE: PatentIn version 3.2
SEGUTH: 60
TYDD: NAM
                                                                             RESULT 10
US-09-422-985-1
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US-10-001-073A-55
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         APPLICANT:
APPLICANT:
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                                               Sequence 1, Application US/09422985 GENERAL INFORMATION:
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; ORGANISM: Homo sapiens
US-09-692-077D-25
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CURRENT FILING DATE: 2001-11-01
NUMBER OF SEQ ID NOS: 69
SOFTWARE: PatentIn version 3.2
SEQ ID NO 55
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Best Local S
Matches 49
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APPLICANT: Liggett, Stephen
TITLE OF INVENTION: Alpha-2 Adrenergic Receptor Polymorphisms
FILE REFERENCE: 10738-42
                                                                                                                                                                                                                                                       LENGTH: 60
TYPE: DNA
ORGANISM: Homo sapiens
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Local Similarity 100.0%; Pred. No. 0.0
hes 49; Conservative 0; Mismatches
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Snapir, Amır
Heinonen, Paul
Alhopuro, Pia
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                     Paula
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100.0%; Pred. No. 0.(
tive 0; Mismatches
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    OCATION:
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NUMBER OF SEQ ID NOS: 10
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 1
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SEQ ID NO 1
LENGTH: 1344
                                                                                       LENGTH: 1344
TYPE: DNA
ORGANISM: Homo
                                                                                                                                                                                                                APPLICANT: Kauhanen, Jussi
APPLICANT: Valkonen, Veli-Pekka
TITLE OF INVENTION: A DNA molecule encoding a variant alpha-2B-adrenoceptor
TITLE OF INVENTION: protein, and uses thereof
FILE REFERENCE: Alpha-2B-AR variant
CURRENT APPLICATION NUMBER: US/99/825,923
CURRENT FILING DATE: 2001-04-05
PRIOR APPLICATION NUMBER: 09/422,985
PRIOR APPLICATION NUMBER: 09/422,985
PRIOR FILING DATE: 2000-05-25
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                                                  FEATURE:
NAME/KEY: CDS
  OTHER INFORMATION: Coding sequence
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APPLICANT: Nyyss'nen, Kristiina
APPLICANT: Salomen, Riitta.
APPLICANT: Salomen, Riitta.
APPLICANT: Kauhanen, Jussi
APPLICANT: Valkonen, Veli-Pekka
TITLE OF INVENTION: A DNA molecule encoding a variant alpha-2B-adrenoceptor
TITLE OF INVENTION: protein, and uses thereof
FILE REFERENCE: Alpha-2B-AR variant
CURRENT APPLICATION NUMBER: US/09/422,985
CURRENT FILING DATE: 199-10-22
COURRENCE SEQ ID NOS: 10
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FEATURE:
NAME/KEY: CDS
LOCATION: (1)..(1341)
OTHER INFORMATION: Coding sequence for variant human
OTHER INFORMATION: alpha-2B-adrenoceptor protein
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1 Similarity 96.1%;
49; Conservati
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Salonen, Riitta
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Salonen, Jukka T
Tuomainen, Tomi-Pekka
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Pesonen, Ullamari
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Scheinin, Mika
Salonen, Jukka T
Tuomainen, Tomi-Pekka
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Koulu, Markku
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for variant human
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RESULT 13
US-10-311-455-47
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-10-077-870-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 47, Application US/10311455
GENERAL INFORMATION:
APPLICANT: OLEK, Alexander
                                                                                                                                                                  NUMBER OF SEQ ID NOS: 2424
SEQ ID NO 47
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CURRENT APPLICATION NUMBER: US/10/077,870
CURRENT FILING DATE: 2002-05-21
PRIOR APPLICATION NUMBER: FI 20010323
PRIOR FILING DATE: 2001-02-20
NUMBER OF SEQ ID NOS: 10
                                                                                                                                                                                                   PRIOR APPLICATION NUMBER: DE 10032529.7
PRIOR FILING DATE: 2000-06-30
PRIOR APPLICATION NUMBER: DE 10043826.1
PRIOR FILING DATE: 2000-09-01
                                                                                                                                                                                                                                                                            CURRENT FILING DATE: 2002-12-16
PRIOR APPLICATION NUMBER: PCT/EP01/07537
PRIOR FILING DATE: 2001-07-02
                                                                                                                                                                                                                                                                                                                             TITLE OF INVENTION: Diagnosis of Diseases Associated with the Immune System by Determ TITLE OF INVENTION: Cytosine methylation FILE REFERENCE: 5013.1014 CURRENT APPLICATION NUMBER: US/10/311,455
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NAME/KEY: CDS
LOCATION: (1).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      OTHER INFORMATION: Coding sequence for variant human alpha-2B-adrenoceptor protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: DNA
ORGANISM: Homo sapiens
                                                                        OTHER INFORMATION:
                                                                                           FEATURE:
                                                                                                           DRGANISM: Artificial Sequence
                     JAME/KEY: unsure
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ENGTH: 1344
                                                                                                                                               ENGTH: 6904
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                                                                                                                                                                                                                                                                                                                                                                                                                           PIEPENBROCK, Christian
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                                                                      chemically treated genomic DNA (Homo sapiens)
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Search completed: March Job time : 2889 secs
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US-60-164-763-274
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Best Local S
Matches 44
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GENERAL INFORMATION:
APPLICANT: Bonazzi, Vivien
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 274
LENGTH: 481
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                                                                                                                                                                                                                                                                            TITLE OF INVENTION: ISOLATED HUMAN GPCR PROTEIN, TITLE OF INVENTION: ACID MOLECULES ENCODING HUMA FILE REFERENCE: CLO00162
CURRENT APPLICATION NUMBER: US/60/169,842
CURRENT FILING DATE: 1999-12-09
NUMBER OF SEQ ID NOS: 5232
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CURRENT APPLICATION NUMBER: US/60/164,763
CURRENT FILING DATE: 1999-11-12
NUMBER OF SEQ ID NOS: 1154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TITLE OF INVENTION: ISOLATED HUMAN GPCR PROTEIN, NUCLEIC TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN GPCR PROTEINS FILE REFERENCE: CL000140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Bonazzi, Vivien
                                                                                                                                                                                                                TYPE: DNA
ORGANISM: Human
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                                                                                                                                                                                                                                               LENGTH: 481
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                                                                                                                               44; Conservative
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Pred. No. 3.1;
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Match Length
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1: /cgn2_6/ptodata/1/pna/US06_NEW_COMB.Beq:*

2: /cgn2_6/ptodata/1/pna/US07_NEW_COMB.Beq:*

3: /cgn2_6/ptodata/1/pna/US07_NEW_COMB.Beq:*

4: /cgn2_6/ptodata/1/pna/US08_NEW_COMB.Beq:*

5: /cgn2_6/ptodata/1/pna/US08_NEW_COMB.Beq:*

6: /cgn2_6/ptodata/1/pna/US09_NEW_COMB.Beq:*

7: /cgn2_6/ptodata/1/pna/US09_NEW_COMB.Beq:*
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PCT-US04-02188-20
PCT-US03-32805-1
US-10-767-701-29063
US-10-767-701-26619
US-10-417-375A-79
US-10-767-701-26619
US-10-767-701-2619
US-10-767-701-2619
US-10-767-701-375A-79
US-10-417-375A-63
US-10-767-701-24209
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Sequence 20, Appli
Sequence 1, Appli
Sequence 29063, A
Sequence 125, App
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Sequence
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Sequence
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Sequence 128, App
Sequence 13517, A
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          79, Appl
15708, A
10555, A
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1057, Appl
167, Appl
167, Appl
23701, A
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7, Appl
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31476, A
2490, Ap
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Sequence 10615,	Sequence 10820,	Sequence 13851	Sequence 11456	Sequence 10125	Sequence 13518	Sequence 14185	Sequence 3854	Sequence 10616	Sequence 72,	Sequence 10632,	Sequence 39,	Sequence 39,	Sequence 13537	Sequence 20232	Sequence 1864	Sequence 10700	Sequence 14827	sequence 's'
515, F	20, A	51, A	56, A	25, A	18, A	95, A	4, Ap	16, A	72, Appl	32, A	Appl	39, Appl	37, A	32, A	4, Ap	00, A	27, A	ישקירי וניי

## ALIGNMENTS

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US-10-417-375A-128/c

; Sequence 128, Application US/10417375A
; GENERAL INFORMATION:
    APPLICANT: David W. Morris
    APPLICANT: Marc Malandro
    TITLE OF INVENTION: Novel Therapeutic Targets in
    FILE REFERENCE: 529452001600
; CURRENT APPLICATION NUMBER: US/10/417,375A
; CURRENT FILING DATE: 2003-04-15
; NUMBER OF ESQ ID NOS: 176
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 128
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TYPE: DNA
; ORGANISM: Saccharomyces cerevisiae
US-10-451-467A-261
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 261, Application US/10451467A GENERAL INFORMATION: APPLICANT: CONTRERAS, ROLAND HENRI APPLICANT: EBERHARDT, INES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 1
US-10-451-467A-261/c
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Best Local Similarity
Matches 38; Conserv
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PRIOR FILING DATE: 2000-12-22
PRIOR APPLICATION NUMBER: EP 01870002.1
PRIOR FILING DATE: 2001-01-04
PRIOR APPLICATION NUMBER: EP 01870003.9
PRIOR FILING DATE: 2001-01-09
NUMBER OF SEQ ID NOS: 732
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APPLICANT: REEKWANS, RIEKA JOSEPHINA
TITLE OF INVENTION: BAX-RESPONSIVE GENES FOR DRUG TARGET IDENTIFICATION
TITLE OF INVENTION: YEAST AND FUNGI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILE REFERENCE: JAB-1667
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84.4%; Pred. No. 0.
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LENGTH: 430442

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CURRENT APPLICATION NUMBER: PCT/US04/02188
CURRENT FILING DATE: 2004-01-23
PRIOR APPLICATION UNMBER: 60/442,582
PRIOR FILING DATE: 2003-01-24
NUMBER OF SEQ ID NOS: 191
SOPTWARE: Patentin version 3.2
SEQ ID NO 20
LENGTH: 3994
TYPE: DNA
ORGANISM: Homo sapiens
PCT-US04-02188-20
        <sup>7</sup>₽
                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 4
PCT-US04-02188-20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; OTHER INFORMATION: Clone ID: SORBI-28MAY03-CLUS447_1 US-10-767-701-13517
                                                                 Query Match
Best Local Similarity
Matches 37; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-417-375A-128
                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CURRENT APPLICATION NUMBER: US/10/767,701
CURRENT FILING DATE: 2004-01-29
NUMBER OF SEQ ID NOS: 63128
SEQ ID NO 13517
LENGTH: 1330
TYPE: DNA
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                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Bayer Pharmaceuticals Corporation APPLICANT: Eveleigh, Deepa APPLICANT: Bigwood, Douglas APPLICANT: Taylor, Ian
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                   TILE REFERENCE: 5151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Kovalic, David K.
APPLICANT: Zhou, Yihua
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof For Plant Improvement
FILE REFERENCE: 38-21 (53535) B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches
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                                                                                                                                                                                                                                                                                                                   PPLICANT: Taylor, Ian
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local
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258 GAĞGATGAAGATĞGCGAĞGAĞGAĞĞAĞĞAĞAĞAAĞAAĞAAĞA 302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 GAGGATGAAGCTGAAGAGGAGGAGGAGGAGGAAGAGTGTGAA 45
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1 Similarity 82.2%;
37; Conservative
                        GAGGATGAAGCTGAAGAGGAGGAGGAGGAGGAGGAGGAGGTGTGAA 45
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                                                                        Conservative
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                                                                                      63.1%;
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80.9%;
                                                                             Score 32.2; DB 1; Length 3994; Pred. No. 0.18;
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                                                                   Mismatches
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; ORGANISM: Homo sapiens
US-10-764-425-20
                                                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQ ID NOS: 535
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 1
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US-10-764-425-20
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APPLICANT: deCODE genetics ehf.
APPLICANT: Helgadottir
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PRIOR FILING DATE: 2003-01-24
NUMBER OF SEQ ID NOS: 191
SOFTWARE: PATENTIN VEYBION 3.2
SEQ ID NO 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CURRENT APPLICATION NUMBER: PCT/US03/32805
CURRENT FILING DATE: 2003-10-16
PRIOR APPLICATION NUMBER: 60/419,432
PRIOR FILING DATE: 2002-10-17
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Best Local Similarity 82.2%;
Matches 37; Conservative
                                               FEATURE:

NAME/KEY: misc_feature
LOCATION: (269991)...(270091)
OTHER_INFORMATION: n = A,T,C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TITLE OF INVENTION: Susceptibility Gene for Myocardial TITLE OF INVENTION: Infarction FILE REFERENCE: 2345.2048002
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                                                                                                                                                                                               NAME/KEY: misc feature
LOCATION: (154988)...(155087)
OTHER INFORMATION: n = A,T,C or G
NAME/KEY: misc_feature
LOCATION: (272544)...(272643)
                                                                                                                               OTHER INFORMATION: n = A,T,C
                                                                                                                                                                                                                                                                             FEATURE:

NAME/KEY: misc_feature
LOCATION: (70677)...(70776)
OTHER_INFORMATION: n = A,T,C or G
                                                                                                                                                                                                                                                                                                                                                         LENGTH: 398800
TYPE: DNA
ORGANISM: homo sapiens
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                                                                                                                                                     NAME/KEY: misc feature
LOCATION: 248521
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FITLE OF INVENTION: EXPRESSION PROFILES FOR COLON CANCER AND METHODS OF USE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LENGTH: 3994
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Gulcher, Jeffrey R.
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Pred. No. 0.18;
0; Mismatches 8;
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OTHER INFORMATION: n = A,T,C or

(279644)

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NAME/KEY: misc\_feature LOCATION: (279545)...( OTHER INFORMATION: n = A,T,C or

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                                                                       ; TYPE: DNA
; ORGANISM: Sorghum bicolor
; FEATURE:
; OTHER INFORMATION: Clone ID:
US-10-767-701-29063
                                                                                                                                                                                                                                                                                                                                                                                                                        US-10-767-701-29063/c
                                                                                                                                                               APPLICANT: KOVALIC, David K.
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof For Plant Improvement
FILE REFERENCE: 38-21(53535)B
CURRENT APPLICATION NUMBER: US/10/767,701
CURRENT APPLICATION ON UNMBER: US/10/767,701
CURRENT FILING DATE: 2004-01-29
NUMBER OF SEQ ID NOS: 63128
SEQ ID NO 29063
LENGTH: 353
TYPEF. NAS
Query Match
Best Local Similarity
Matches 36; Conserv
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LOCATION: (396625)...(396724)
OTHER INFORMATION: n = A,T, C or G
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LOCATION: (391524)...(391623)
OTHER INFORMATION: n = A,T,C or
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LOCATION: (345190)...(345289)
OTHER_INFORMATION: n = A,T,C or G
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LOCATION: (327555)...(327654)
OTHER INFORMATION: n = A,T,C or G
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LOCATION: (300892)...(300991)
OTHER INFORMATION: n = A,T,C or G
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LOCATION: (350504)...(350603)
OTHER INFORMATION: n = A,T,C or G
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LOCATION: (341698)...(341698)
OTHER INFORMATION: n = A,T,C or
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LOCATION: (332849)...(332948)
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   Conservative
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                 61.2%;
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Score 31.2; DB 6;
Pred. No. 0.27;
0; Mismatches 8;
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Pred. No. 0.28;
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                                     Length 353;
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Gaps
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RESULT 10
US-10-767-701-26619/c
US-10-767-701-26619/c
; Sequence 26619, Application US/10767701
; GENERAL INFORWATION:
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
                                                                                                                                                                                                                                                                                      ; FEATURE:

; NAME/KEY: misc feature

; LOCATION: (1)...(209320)

; OTHER INFORMATION: n = A,T,C or G,

US-10-767-471-10681
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CURRENT FILING DATE: 2004-01-30
NUMBER OF SEQ ID NOS: 50231
SOFTWARE: FASESEQ for Windows Version 4.0
SEQ ID NO 10681
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 10681, Application US/10767471
GENERAL INFORMATION:
APPLICANT: CARGILL, Michele et al.
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Best Local Similarity
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Best Local Similarity
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APPLICANT: Marc Malandro
TITLE OF INVENTION: Novel Therapeutic Targets
FILE REFERENCE: 529452001600
CURRENT APPLICATION NUMBER: US/10/417,375A
CURRENT FILING DATE: 2003-04-15
NUMBER OF SEQ ID NOS: 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: CARGILL, Michele et al.
TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
TITLE OF INVENTION: RHEUMATOID ARTHRITIS, METHODS OF DET.
FILE REFERENCE: CL001505
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME/KEY: misc feature
LOCATION: (1)...(188053)
OTHER INFORMATION: n = A,T,C or
                                                                                                                                                                                                                                                                                                                                                                              ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: DNA
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                                                                                                                                                                                                                                                                                                                                                                                                                  ENGTH:
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Pred. No. 0.
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Pred. No. 0.5;
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US-10-417-375A-79/c
; Sequence 79, Application US/10417375A
; GENERAL INFORMATION:
; APPLICANT: David W. Morris
APPLICANT: Marc Malandro
; TITLE OF INVENTION: Novel Therapeutic Targets in Cancer
; FILE REFERENCE: 529452001600
; CURRENT APPLICATION NUMBER: US/10/417,375A
; CURRENT FILING DATE: 2003-04-15
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Best Local Similarity
Matches 34; Conserva
                                                                                 CURRENT FILING DATE: 2003-04-15
NUMBER OF SEQ ID NOS: 176
SOFTWARE: FRAELSEQ for Windows Version 4.0
SEQ ID NO 1
LENGTH: 310122
                                                                                                                                                                                                                                                                                                                                                                                                                                          ; TYPE: DNA
; ORGANISM: Mus musculus
US-10-417-375A-79
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CURRENT APPLICATION NUMBER: US/10/767,701
NUMBER OF SEQ ID NOS: 63128
SEQ ID NO 26619
LENGTH: 650
TYPE: DNA
ORGANTED.
                                                                                                                                                                       APPLICANT: David W. Morris
APPLICANT: Marc Malandro
TITLE OF INVENTION: Novel Therapeutic Targets
FILE REFERENCE: 529452001600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQ ID NOS: 176
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 79
LENGTH: 54303
      FEATURE:

NAME/KEY: misc_feature
LOCATION: (1)...(310122
OTHER INFORMATION: n =
                                                                                                                                                          CURRENT APPLICATION NUMBER: US/10/417,375A
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                                                                ORGANISM: Mus musculus
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RESULT 15 US-10-642-946-6

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; Sequence 6, Application US/10642946

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FILE REFERENCE: CL001505

CURRENT APPLICATION NUMBER: US/10/767,471

CURRENT FILING DATE: 2004-01-30

NUMBER OF SEQ ID NOS: 50231

SOFTWARE: FASTSEQ for Windows Version 4.0

SEQ ID NO 10555

LENGTH: 34304
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 10555, Application US/10767471
GENERAL INFORMATION:
APPLICANT: CARGILL, Michele et al.
TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
TITLE OF INVENTION: RHEUMATOID ARTHRITIS, METHODS OF DETECTION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Kovalic, David K.
APPLICANT: Zhou, Yihua
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
FILE REFERENCE: 38-21(5353)B
CURRENT APPLICATION NUMBER: US/10/767,701
CURRENT FILING DATE: 2004-01-29
SEQ ID NO 15708
LENGTH: 940
TYPE: DNA
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US-10-767-701-15708/c
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OTHER INFORMATION: n = A,T,C or G, or insertion/deletion polymorphism (see Tables
                                                                                                                                                                                                                                                                                             NAME/KEY: misc_feature LOCATION: (1)...(34304
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TYPE: DNA
ORGANISM: Homo sapiens
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Best Local Similarity
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                                   1 GAGGATGAAGCTGAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAA 45
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87.2%;
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Pred. No. 0.62;
0; Mismatches
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Pred. No. 0.59;
0; Mismatches 5; Indels 0
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GENERAL INFORMATION:

APPLICANT: Ryan; James W.

TITLE OF INVENTION: Genomic Polynucleotide Fragments From Chromosome 7

FILE REFERENCE: JR-14,000-US

CURRENT APPLICATION NUMBER: US/10/642,946

CURRENT FILING DATE: 2003-08-18

PRIOR APPLICATION NUMBER: US/09/957,956

PRIOR FILING DATE: 2001-09-21

NUMBER OF SEQ ID NOS: 8

SOFTWARE: Patentin version 3.1

SEQ ID NO 6

LENGTH: 45980

TYPE: DNA

OCANISM: Homo sapiens

US-10-642-946-6

Query Match
Seet Local Similarity 80.0%; Pred. No. 0.64;
Best Local Similarity 80
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B 74.1 633 9 ALB72808 ALB72808 B 74.1 634 9 ALB52740 ALB52740 ALB52740 ALB728077 72.5 642 14 CF360731 CF360737 CF360737 72.5 642 14 CF360731 CF360737 CF360737 72.5 787 13 BU748295 BU748295 77.0 728 BZ195097 CR315228 CF3625989 CF3625867 CF362587 CF36258	AL848797 AL84	٠.	49	.2	4.8 6	
B 74.1 633 9 ALB72808 ALB72808 74.1 634 9 ALB52740 ALB52740 ALB52740 ALB728077 72.5 642 14 CF360731 CF360737 72.5 642 14 CF360731 CF360737 72.5 787 13 BU748295 BU748295 771.0 256 14 CA315228 CA315228 AAB96321 AAB9632 AAB96321 AAB9632 AAB96321 AAB96321 AAB96321 AAB96321 AAB9632 AAB	AL652867 AL65		48	2	4.8 6	
8 74.1 633 9 ALB72808 ALB72808 8 74.1 634 9 ALB52740 ALB52740 ALB52740 ALB728077 72.5 642 14 CF360731 CF360737 CF360737 72.5 787 13 BU748295 BU748295 71.0 256 14 CR315228 CR315228 CR315228 71.0 256 14 CR315228 CR31528 CR	AL791191 AL79	٠.	64	.2	4.8 6	
B 74.1 633 9 ALB72808 ALB72808 ALB72808 ALB72808 ALB72808 ALB72808 ALB72807	AL308675 Tet		9	.6 10	5	
8 74.1 633 9 AL872808 8 74.1 634 9 AL852740 7 72.5 642 14 CF360731 7 72.5 642 14 CF360731 7 72.5 642 14 CF360731 7 72.5 787 13 BU748295 7 71.0 256 14 CA315228 7 70.6 490 9 AA896321 6 70.6 822 14 CB625999 6 70.6 822 12 BM655999 6 70.6 822 12 BM655999 6 9.4 365 12 BM655999 6 9.4 399 12 BI961415 6 9.4 446 12 BI961033 6 9.4 446 12 BI961033 6 69.4 496 10 AW760336 6 69.4 497 9 AL842491 4 69.4 512 14 CF795982 6 69.4 552 14 CF795982 6 69.4 552 13 BX676418 6 69.4 552 13 BX676418 6 6 6 6 6 7 13 BX706040 6 6 7 6 7 13 BX706040 6 6 7 6 7 13 BX706040 6 6 7 1 1 AK000590 6 8 6 6 6 6 17 10 BF220168 6 7 1	AW388194 MR4		27	.6	5	
8 74.1 633 9 ALB72808 ALB72808 8 74.1 634 9 ALB52740 ALB52740 ALB52740 ALB728077 APA 5.24 APA	BF220068 601		17	6	5	
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8 74.1 633 9 AL872808 8 74.1 634 9 AL872808 8 74.1 634 9 AL852740 7 72.5 642 14 CF360731 7 72.5 787 13 BU748295 7 71.0 256 14 CA315228 7 71.0 256 14 CA315228 7 70.6 490 9 AR896321 6 70.6 822 14 CB625999 6 70.6 822 14 CB625999 6 70.6 822 14 CB625990 6 9.4 365 12 BM655898 6 9.4 399 12 BI961033 4 69.4 399 12 BI961033 4 69.4 446 12 BI961033 4 69.4 446 12 BI961033 4 69.4 496 10 AW760336 6 9.4 552 14 CF959982 7 CF95982 7 CF959336 7 CF959336 7 CF959336 7 CF959336 7 CF959336 7 CF959336 7 CF95934 7 CF959336 7 CF95934 7 CF9594 7 CF95	AK008242 Mus		95	.4 15	5.4 6	
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B 74.1 633 9 ALB72808 ALB72808 ALB72808 ALB72808 ALB72808 ALB728077 ALB52740 ALB52750 ALB5280 A	BZ504700 BON		23	. <u>4</u> .	5.4 6	
8 74.1     633     9 AL872808     AL872808       74.1     634     9 AL852740     AL852740       7 72.5     642     14 CF360731     CF36071       7 72.5     642     14 CF360731     BU748295       7 72.5     787     13 BU748295     BU748295       7 71.0     70.6     14 CA315528     CA31522       7 70.6     490     9 AA896321     CA3152       7 70.6     822     14 CB625990     CB62591       6 9.4     365     12 BM659898     BM659898       4 69.4     399     12 BI961415     BI9614       4 69.4     496     12 BI961033     BL96103       4 69.4     496     10 AW760336     BL96103       4 69.4     496     10 AW760336     CB27293       4 69.4     496     13 BX676618     AW7603       4 69.4     552     14 CF795982     CF79523       4 69.4     571     13 BX676618     BX6764       4 69.4     69.4     69.4     CF795361       4 69.4     69.4     69.4     CF795234	BY706040 BY7		77	.4	5.4 6	
B 74.1 633 9 AL872808 AL872808 AL872808 AL872808 AL872808 AL872808 AL872808 AL872808 AL8728077 AL872877 AL85274 AL852740 AL852740 AL852740 AL852740 AL852740 AL852740 AL852740 AL852740 AL852740 AL85275 AL87280 AL872	CF792336 885		73	.4	5.4 6	
8 74.1     633     9 AL872808     AL87280       8 74.1     634     9 AL852740     AL852740       7 72.5     642     14 CF360731     CF36073       7 72.5     787     13 BU748295     BU748295       7 71.4     770     28 BZ19597     B219597       2 71.0     256     14 CB452589     CA31522       6 70.6     490     9 AA896321     CB625989       7 70.6     763     14 CB625989     CB62599       6 70.6     822     14 CB625999     CB62599       6 70.6     822     12 BM659998     BM6598       4 69.4     365     12 BM659998     BM6598       4 69.4     399     12 B1961033     B196103       4 69.4     446     12 B1961033     B196103       4 69.4     446     12 B1961033     B19610449       4 69.4     446     12 B1961033     B19610       4 69.4     497     PAL842491     AU760336     AU760336       4 69.4     512     14 CB795982     CB7959       4 69.4     512     14 CB795982     CB7959       4 69.4     512     13 BX669429     BX6694       4 69.4     571     13 BX67644     BX66764       4 69.4     586     9 A1451753	CF367914 852		80	.4	σ	
8 74.1     633     9 AL872808     AL872808       8 74.1     634     9 AL852740     AL852740       7 72.5     642     14 CF360731     CF36073       7 72.5     787     13 BU748295     BU748295       7 71.4     770.5     8 BZ195097     BZ195097       2 71.0     256     14 CA315228     CA31522       6 70.6     490     9 AA896321     CA32590       6 70.6     822     14 CB625989     CB6259       6 70.6     822     14 CB625990     CB6259       6 70.6     822     14 CB625990     CB6259       6 70.4     365     12 BM659898     BQ594503       4 69.4     399     12 BI961415     B196103       4 69.4     399     12 BI961415     B19610       4 69.4     496     12 BI961033     AL842491       4 69.4     496     10 AW760336     AL978633       4 69.4     512     14 CB272922     CB2729       4 69.4     512     14 CB795982     CB7759       4 69.4     552     14 CF7959982     CW77599       4 69.4     552     14 CB77959982     CW7859982       4 69.4     552     14 CB77959982     CW7859982       4 69.4     552     13 BX676418 <td< td=""><td>AI451753 mb16</td><td>٠.</td><td>86</td><td>4.</td><td>5.4 6</td><td></td></td<>	AI451753 mb16	٠.	86	4.	5.4 6	
8 74.1     633     9 AL872808     AL872808       8 74.1     634     9 AL852740     AL852741       7 72.5     642     14 CF360731     CP36073       7 72.5     787     13 BU748295     BU748295       4 71.0     228 BZ195097     BZ195097       2 71.0     226 14 CR315528     AA896321       6 70.6     490     9 AA896321     CA3152       6 70.6     763 11 CB625999     CB62599     CB6259       6 70.6     822 14 CB625990     CB6259     CB6259       6 70.6     822 14 CB625990     CB6259     CB6259       6 9.4     378 13 BQ294503     BQ294503     B1961013       4 69.4     399 12 B1961013     B1961013     B196104       4 69.4     447 9 AL842491     AL84249     AL84249       4 69.4     496 10 AW760336     AW7603     AW7603       4 69.4     552 14 CB795982     CB27959       4 69.4     556 13 BX669429     BX6694	BX676418 BX6		71	4.	5.4 6	
B 74.1 633 9 AL872808 AL872808 AL872808 AL872808 AL872808 AL872807 AL852740 AL85275 AL85280 AL852	BX669429 BX6		56	4.	5.4 6	
8 74.1     633     9 AL872808     AL87280       8 74.1     634     9 AL852740     AL852740       7 72.5     642     14 CF360731     CF36073       7 72.5     787     13 BU748295     BU748295       7 71.4     770.2     8 BZ195097     BZ195097       2 71.0     256     14 CA315228     CA31522       2 70.6     490     9 AA896321     CB625989       6 70.6     822     14 CB625989     CB62599       6 70.6     822     14 CB625990     CB62590       6 70.6     822     14 CB625990     CB6259       6 9.4     365     12 BM659898     BQ294503       4 69.4     399     13 BQ294503     BQ294503       4 69.4     399     13 B1961033     B196103       4 69.4     446     12 B1961033     B19610       4 69.4     496     10 AW760336     BL94343       4 69.4     496     10 AW760336     AL842491       4 69.4     496     10 AW760336     AL862799       4 69.4     496     10 AW760336     AL86279       4 69.4     496     10 AW760336     AL86279       4 69.4     496     10 AW760336     AU602424       4 69.4     496     10 AW760336     AU6	CF795982 892		52	4.	5.4 6	
8 74.1     633     9 AL872808     AL872808       8 74.1     634     9 AL852740     AL852740       8 74.1     634     9 AL852740     CP360731     CP36077       7 72.5     642     14 CP360731     CP36073     BU748295     BU748295       7 72.5     787     13 BU748295     BU748295     BU748295       4 71.4     770     28 BZ195097     BZ195097     BZ195097       2 71.0     256     14 CR3155228     CA31522       6 70.6     490     9 AA896321     CA382591     CA382591       6 70.6     822     14 CB625999     CB62591     CB62591       6 70.6     822     14 CB625990     CB62591     CB62591       6 9.4     378     13 BQ294503     BU65294       4 69.4     399     12 BU961415     BU96141       4 69.4     447     9 AL8424291     BL96141       4 69.4     447     9 AL8424291     AL8424291       4 69.4     496     10 AW760336     AL9476033	CB272922 mai		12	4.	5.4 6	
8 74.1     633     9 AL872808     AL872808       74.1     634     9 AL852740     AL852740       7 72.5     642     14 CF360731     CF36073       7 72.5     787     13 BU748295     BU748295       7 71.4     770     28 BZ195097     BZ195097       2 71.0     256     14 CA315228     CA31522       6 70.6     490     9 AA896331     CB625989       6 70.6     763     14 CB625989     CB62599       6 70.6     822     14 CB625989     CB62599       4 69.4     365     12 BM6559898     BM65598       4 69.4     378     13 BQ294503     BQ2945       4 69.4     446     12 BI961013     B196101       4 69.4     446     12 BI96103     B196124       4 69.4     447     9 AL842491     AL442491	AW760336 sl4		96	.4	5.4 6	
8     74.1     633     9     AL872808     AL87280       8     74.1     634     9     AL852740     AL852740       7     72.5     642     14     CF360731     CF36073       7     72.5     642     14     CF360731     BU748295       7     72.5     787     13     BU748295     BU748295       7     71.4     770     28     BZ195097     BZ195097       2     71.0     256     14     CB315228     CA31522       6     70.6     490     9     AA896321     CB62591       6     70.6     763     14     CB625990     CB62590       6     70.6     822     14     CB625990     CB62591       6     70.6     822     14     CB625990     CB62591       6     70.6     822     BM659998     BM65981       4     69.4     365     12     BM659998     BM65981       4     69.4     399     13     BU294503     BU294503       4     69.4     446     12     BU961033     B196103	AL842491 AL84	٠.	47	.4	5.4 6	
8 74.1     633     9 AL872808     AL87280       8 74.1     634     9 AL852740     AL852740       8 74.1     634     9 AL852740     CP360731       7 72.5     642     14 CP360731     CP36073       7 72.5     787     13 BU748295     BU748295       4 71.0     228 BZ195097     BZ195097     BZ195097       2 71.0     256 14 CR3155228     CA31522       6 70.6     490     9 AA896321     CA3896321       6 70.6     763     14 CB625590     CB62591       6 70.6     822     14 CB625590     CB62591       6 70.6     822     14 CB625909     CB62591       6 69.4     378     13 BQ294503     BQ629450       4 69.4     378     13 BQ294503     BQ294503       4 69.4     399     12 BI961415     B1961415	BI961033 MON		46	. 4 4	5.4 6	
8     74.1     633     9     AL872808     AL872808       8     74.1     634     9     AL852740     AL852740       8     74.1     634     14     CF360731     CF360731       9     72.5     642     14     CF360731     BU748295       9     71.4     770     28     BZ195097     BZ195097       10     256     14     CA315228     CA31522       10     70.6     490     9     AA896331     AA896331       10     70.6     70.6     14     CB625989     CB62591       10     69.4     365     12     BM659898     BM65989       4     69.4     378     13     BQ294503     BQ294503	BI961415 MON		99	٠ <u>.</u> ٤٠	5.4	
8     74.1     633     9     AL872808     AL87280       8     74.1     634     9     AL852740     AL852741       7     72.5     642     14     CF360731     CF36073       7     72.5     787     13     BU748295     BU748295       7     71.4     770     28     BZ195097     BZ195097       2     71.0     256     14     CA315228     CA31522       6     70.6     490     9     AA896321     AA896321       6     70.6     763     14     CB625998     CB62599       6     70.6     822     14     CB625990     CB62590       4     69.4     365     12     BM659998     BM65998	BQ294503 Pa0		78	4.	5.4 6	
8     74.1     633     9     AL872808     AL87280       8     74.1     634     9     AL852740     AL852740       8     74.1     634     9     AL852740     CP360731     CP36073       7     72.5     642     14     CP360731     BU748295     BU748295       4     71.4     770     28     BZ195097     BZ19509       2     71.0     256     14     CA315528     CA3152       6     70.6     490     9     AA896321     AA896329       6     70.6     763     14     CB625990     CB62599       6     70.6     822     14     CB625990     CB62599	BM659898 BJP		85	4.	5.4 6	
B     74.1     633     9     AL872808     AL872808       A1     634     9     AL852740     AL852741       7     71.1     642     14     CF360731     CF36073       7     72.5     787     13     BU748295     BU748295       4     71.4     770     28     BZ195097     BZ19509       7     71.0     256     14     CA315228     CA315228       6     70.6     490     9     AA896321     AA896321       6     70.6     763     14     CB625989     CB62599	CB625990 OSI		22	6	6 7	
8 74.1     633     9 AL872808     AL872808       8 74.1     634     9 AL852740     AL852740       7 72.5     642     14 CF360731     CF36071       7 72.5     7 72.5     13 BU748295     BU748295       7 71.4     770     28 BZ195097     BZ195097       2 71.0     256     14 CA315228     CA31522       6 70.6     490     9 AA896331     AA89632	CB625989 OSI		3	6	6 7	
8     74.1     633     9     AL872808     AL87280       8     74.1     634     9     AL852740     AL852740       7     72.5     642     14     CF360731     CF3607.       7     72.5     787     13     BU748295     BU748295       4     71.4     770     28     BZ195097     BZ195097       2     71.0     256     14     CA3155228     CA31522	AA896321 vy13	٠.	90	.6	6 7	
8     74.1     633     9     AL872808     AL872808       74.1     634     9     AL852740     AL852740       7     72.5     642     14     CF360731     CF3607.       7     72.5     787     13     BU748295     BU7482.       4     71.4     770     28     BZ195097     BZ195097	CA315228 UI-		56	.0	2 7	
8     74.1     633     9     AL872808     AL87280       8     74.1     634     9     AL852740     AL852741       7     72.5     642     14     CF360731     CF36071       7     72.5     787     13     BU748295     BU74821	BZ195097 CH2		70	.4.	6.4 7	
8 74.1 633 9 AL872808 AL872808 AL87 8 74.1 634 9 AL852740 AL852740 AL85 7 72.5 642 14 CF360731 CF360731 822	BU748295 CH3		87	5	7 7	
8 74.1 633 9 AL872808 AL872808 AL8 8 74.1 634 9 AL852740 AL852740 AL8	CF360731 822		42	.5	7 7	
8 74.1 633 9 AL872808 AL872808 AL87	587	٠.	34	.1	7	
	L87	٠.	S	σ.	7.8	

## ALIGNMENTS

ACCESSION VERSION KEYWORDS SOURCE ORGANISM RESULT 1
AY416856
LOCUS
DEFINITION REFERENCE AUTHORS REFERENCE TITLE JOURNAL TITLE AUTHORS PUBMED 14671302
2 (bases 1 to 1353)
Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejariwal, A., Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B., Ferriera, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J., Adams, M.D. and Cargill, M.
Direct Submission 1 (bases 1 to 1353)
Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A., Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B., Terriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J., Adams,M.D. and Cargill,M.
Inferring nonneutral evolution from human-chimp-mouse orthology gene trios Science 302 (5652), 1960-1963 (2003) Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. Homo sapiens AY416856 AY416856.1 Homo sapiens HCM6030 gene, genomic survey sequence. AY416856 Homo sapiens (human) GI:39772816 evolution from human-chimp-mouse orthologous 1353 bp DNA linear GSS 12-DEC-2003

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  Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       44;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive, Rockville, MD 20850, USA
This sequence was made by sequencing genomic exons and ordering them based on alignment.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Dr. James R. Lupski
CDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        BQ880026 1044 bp mRV
AGENCOURT 8113358 Lupski dorsal root clone IMAGE:6179035 5', mRNA sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Plate: LLAM13559
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        http://image.llnl.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BQ880026.1 GI:22272034
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             found through the I.M.A.G.E. Consortium/LLNL at:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens (human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GAAGAGGAGGAGGAGGAGGAGGAAGAGTGTGAACCCCCAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (bases 1 to 1044)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   quality sequence stop: 430.
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                                                                             5'-GACTAGTTCTAGATCGCGAGCGGCCCT(15)-3'. Size selected > 1 kb for average insert length 1.7 kb. This is a primary library, non-amplified. Library constructed by Life Technologies and donated by J. Lupski, M.D./Ph.D. (Baylor College of Medicine) and is available through Life
                                                                                                                                                                                    /clone_lib="Lupski_dorsal_root_ganglion"
/note="Vector: pCNV-SPORT6 (Life Technologies); Si
Not1; Site 2: Sall; cDNA made by oligo-dT priming.
Directionally cloned using the following adaptors:
5'-TCGACCCACGCGTCCG-3' and
                                                              Technologies
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /mol_type="genomic DN
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                         /tissue_type="dorsal root ganglia"
/dev_stage="adult, 36 yr"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                           /organism="Homo sapiens"
/mol type="mRNA"
/db xref="taxon:9606"
/clone="IMAGE:6179035"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /locus_tag="HCM6030"
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                                                                                                                                                                                                                                                                                                                                                          /sex="male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ocation/Qualifiers
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91.7%;
    78.4%;
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  Score
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Pred. No. 1:
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  40;
  DB
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  13;
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_ganglion Homo
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Length 1044;
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SOURCE
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VERSION
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ECAA2BAR
LOCUS
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KEYWORDS
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AY416858
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TITLE
JOURNAL
                                 AUTHORS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AUTHORS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches
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                                                                                                                                                                                                                                                                                                            883
                                                                                                                                                Horse alpha2 adrenergic receptor gene fragment probably genomic survey sequence.
AL606560
AL606560.1 GI:15591917
                                                                                                                                                                                                                                                                                                                                                                           43;
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                                                                                                                                                                                                                                                                                                                                          1 GAGGATGAAGCTGAAGAGGAGGAGGAGGAGGAAGAGTGTGAACCCCA 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2 (bases 1 to 1347)
Clark, A.G., Glanowski, S., Nielson, R., Thomas, P.,
Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F.,
Ferriera, S., Wang, G., Zheng, X.H., White, T.J., Sr
Adams, M.D., and Cargill, M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          gene trios
Science 302 (5652), 1960-1963 (2003)
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Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejariwal, A., Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B., Ferriera, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J., Adams, M.D. and Cargill, M.
              Hunter, C. and Elgar, G. Alpha2 adrenergic rece
                                                                                                    Equus caballus
                                                                                                                                  GSS; Alpha2 adrenergic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This sequence was made by sequencing genomic exons and ordering them based on alignment.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Submitted (16-NOV-2003) Celera Genomics, Rockville, MD 20850, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mus musculus
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                                                                               Eukaryota; Metazoa;
                                                                                                                    Equus caballus (horse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Direct Submission
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                                                                   Mammalia;
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                                               (bases 1 to 872)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         musculus (house mouse)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /organism="Mus musculus"
/mol_type="genomic DNA"
/db_xref="taxon:10090"
                                                                   Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                           locus_tag="HCM6030"
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86.0%;
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               receptor gene
                                                                 Perissodactyla;
                                                                                  Chordata; Craniata; Vertebrata; Euteleostomi;
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Pred. No. 43;
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0; Mismatches
                                                                                                                                  receptor gene
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ne, VIRTUAL
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                                                                                                                                                                                                                                                                                                                                                                         . 7;
                                                                 Equidae; Equus.
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This, Murphy, B.,
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TITLE
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AL872808/c
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 Local Similarity 85.
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AL872808
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Direct Submission

Direct Submission

Submitted (14-SEP-2001) MRC Human Genome Mapping

Centre Hinxton, Cambridge, CB10 1SB. UK Email:
                                                                                                                                                                                                                                                                                                                   constructed by Aaron M. Zorn.

CDNA was oligo dT primed from Sug of poly A+ RNA from EcoRI-NotI cut cDNA was then ligated into pCS107 with 5' end and NotI at the 3' end.

Yector: pCS107; Site 1: EcoRI; Site 2: NotI Host: Escherichia coIi xLI-blue.

Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 (bases 1 to 633)
Croning, M.D.R., Ashurst, J.L., Taylor, R., Zorn, A.M. and Rogers, J. Sanger Xenopus tropicalis EST project 2001 (11_2003)
Unpublished (2003)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 GAGGATGAAGCTGAAGAGGAGGAGGAGGAGGAGAGAGTGTGAACCCCAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sanger Xenopus tropicalis EST project 2001
TROPICALIS SEQUENCE ID: TB99106k18.plkSP6
Sequencing primer: SP6
This sequence is from a Xenopus Gene Collection (XGC)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        On Sep 15, 2002 this sequence version replaced gi:22893073. Contact: Taylor R
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Silurana tropicalis (western clawed frog) Silurana tropicalis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            biohelp@hgmp.mrc.ac.uk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Email: trop@sanger.ac.uk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sanger Institute
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     h 74.9%;
Similarity 84.3%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Cambridgeshire,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              XGC-egg Silurana
                                                                                        /clone_lib="XGC-egg", or 1: EcoRI; Site_2: NotI; cDNA /note="Vector: pCS107; Site_1: EcoRI; Site_2: NotI; cDNA was oligo of primed from 5ug of poly A+ RNA from egg. EcoRI-NotI cut cDNA was then ligated into pCS107 with EcoRI at the 5' end and NotI at the 3' end"
                                                                                                                                                                                                                                                         /organism="Silurana tropicalis"
/mol_type="mRNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /organism="Equus caballus"
/mol_type="genomic DNA"
/db_xref="taxon:9796"
                                                                                                                                                                                                                          /db_xref="taxon:8364"
/clone="TEgg106k18"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ocation/Qualifiers
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               74.1%;
85.7%;
                                                                                                                                                                                     host="Escherichia coli XL1-blue"
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Score 37.8; D
Pred. No. 64;
O; Mismatches
 0
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Pred. No. 5
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tropicalis cDNA clone TEgg106k18
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7;
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                                   Length 633;
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k18 5', mRNA
Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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DEFINITION
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CF360731/c
LOCUS
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AL852740/c
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                                                                                        KEYWORDS
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Best Local Similarity
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                                                                                                    CF360731
CF360731.1
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                                                                                                                                                                                                                                                                                                                     42;
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CDNA was oligo dT primed from Sug of poly A+ RNA ECORI-NotI cut cDNA was then ligated into pCS107 5' end and NotI at the 3' end.

Vector: pCS107; Site 1: ECORI; Site 2: NotI Host: Escherichia coli XL1-blue.
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Eukaryota; Metazoa;
Mammalia; Eutheria;
1 (bases 1 to 642)
                                                     Sus scrofa
                                                                                         EST.
                                                                                                                                       CF360731 642 bp mR
822256 MARC 3PIG Sus scrofa cDNA 3',
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Unpublished (2003)
On Sep 15, 2002 this sequence version replaced gi:22872961
Contact: Taylor R
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Croning, M.D.R., Ashurst, J.L.,
Sanger Xenopus tropicalis EST
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AL852740
                                                                     Sus scrofa (pig)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequencing primer: SP6
This sequence is from a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sanger Xenopus tropicalis EST project 2001
TROPICALIS_SEQUENCE_ID: TEgg015d14.plkSP6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; I
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Silurana tropicalis (western clawed frog)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sanger Institute
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Kenopodinae; Silurana.
                                                                                                                                                                                                                                                                      GAGGATGAAGCTGAAGAGGAGGAGGAGGAGGAGGAGGAGGTGTGAACCCCC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (bases 1 to 634)
                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  trop@sanger.ac.uk
                                                                                                                                                                                                                                                                                                                                                                                                      /clone lib="XGC-egg"
/note="Vector: pCS107; Site 1: EcoRI; Site 2: NotI; cDNA
/note="Vector: pCS107; Site 1: EcoRI, Site 2: NotI; cDNA
was oligo dT primed from 5ug of poly A+ RNĀ from egg.
EcoRI NotI cut cDNA was then ligated into pCS107 with
EcoRI at the 5' end and NotI at the 3' end"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              dev_stage="egg"
/lab_host="Escherichia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ocation/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   clone="TEgg015d14"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      organism="Silurana tropicalis"
                                                                                                        GI:34158729
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                                                                                                                                                                                                                                                                                                                                    74.1%;
85.7%;
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_xref="taxon:8364"
                  Chordata; Craniata; Vertebrata; Cetartiodactyla; Suina; Suidae;
                                                                                                                                                                                                                                                                                                                  ; Score 37.8; D; Pred. No. 64; O; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  coli XL1-blue"
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                                                                                                                                                           mRNA
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                                                                                                                                         mRNA sequence
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into pCS107
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                                                                                                                                                                                                                                                                                                                                                      Length 634;
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                                                                                                                                                                                                                                                                                    49
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9015d14 5', mRNA
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                                      Euteleostomi;
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; Pipidae;
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AUTHORS
TITLE
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BU748295
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ORGANISM
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Matches
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                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.

1 (bases 1 to 787)

Yi, V. Desai,R., Olarte,M., Henthorn,P. and George A.L.

Expressed sequence tags from Canine heart

Unpublished (2003)

Other ESTs: CH3#019 B01T3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BU748295 787 bp mRNA linear EST 10-OCT-2002 CH3#019 B01T7 Canine heart normalized cDNA Library in pBluescript Canis familiaris cDNA clone CH3#019_B01 5', mRNA sequence.
                                                                                                                                                                                                                                                                                           Contact: George AL
Division of Genetic Medicine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Canis familiaris (dog)
Canis familiaris
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 GAGGATGAAGCTGAAGAGGAGGAGGAGGAGGAAGAGTGTGAA 45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           40;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   cross_match v0.990329.
Plate: SRG8014 row: O column: 4
Seq primer: TAGAAGGCACAGTCGAGG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Contact: Smith TPL USDA, ARS, US Meat Animal Research Center PO Box 166, Clay Center, NE 68933-0166, USA Tel: 402 762 4366
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Single pass sequencing. Bases called with phred v0.020425.c and trimmed with the aid of the trim_alt option. Vector identified of the trim_alt option.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Unpublished (2003)
Contact: Smith TPL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Smith, T.P.L., Freking, B.A., Ford, J.J., Vallet, J.L., Fox, J., Wise, T.A., Nonneman, D.J., Wray, J.E. and Keele, J.W.

Necond set of porcine ESTs from a pooled-tissue normalized
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         72.5%;
Similarity 88.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Email: smith@email.marc.usda.gov
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/organism="Canis familiaris"
/mol_type="mRNA"
/db_xref="taxon:9615"
/clone="CH3#019_B01"
                                                                                                  location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /clone lib="MARC 3PIG"
/note="Vector: pcDNA3.1; Site 1: EcoRI; Site 2: NotI;
/hibrary made with RNA pooled from multiple tissues
including brain, liver, muscle, placenta/endometrium,
ovary, testes, and bone marrow."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /mol_type="mRNA"
/db_xref="taxon:9823"
/tissue_type="pooled"
/lab_host="DH10B"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GI:23700479
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AUTHORS
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VERSION
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LOCUS
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Best Local Similarity
                                                                                                                                                                                                                             source
                                                                                                                                                                                                                                                                                                      Email: szhao@tigr.org

Clones are derived from the rat BAC library CHORI-230

(http://www.chori.org/bacpac/rat230.htm). For BAC library

availability, please contact Pieter de Jong (pdejong@mail.cho.org).

Clones may be purchased from BACPAC Resources

(http://www.chori.org/bacpac/or ering_information.htm). BAC end
page: http://www.tigr.org/tdb/bac_ends/rat/bac_end_intro.html

Plate: 248 row: P column: 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Zhao,S., Shetty,J., Shatsman,S., Tsegaye,G., Geer,K., Shvartsbeyn,A., Gebregeorgis,E., Overton,L., Russell,D., (Riggs,F., de Jong,P. and Fraser,C.M. Rat BAC End Sequences from Library CHORI-230 MboI segment Unpublished (199)
Other GSS8: CH230-248P14.TJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   41
                                                                                                                                                                                                                                                                 Seq primer: T7
Class: BAC ends.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Contact: Shaying Zhao
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville,
Tel: 301 838 0208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              40;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Rattus norvegicus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Rattus norvegicus (Norway rat)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BZ195097
BZ195097.1 GI:23853149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CH230-248P14, genomic survey sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CH230-248P14.TV CHORI-230 Segment 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 GAGGATGAAGCTGAAGAGGAGGAGGAGGAGGAGGAGGAGGTGTGAA 45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Rattus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (bases 1 to 770)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
        /cell type="Brain"
/clone_lib="CHORI-230 Segment 2"
/note="Vector: pTARBAC1.3; Site_1: MboI; Site_2: Mb
CHORI-230 Rat (BN/S8NHsd/MCW) BAC library produced
Pieter de Jong"
                                                                                                                 /organism="Rattus norvegicus"
/mol_type="genomic_DNA"
/strain="BN/SsNHsd/MCW"
/db_xref="taxon:10116"
/clone="CH230-248P14"
                                                                                                  /sex="Female"
                                                                                                                                                                                                                             Location/Qualifiers
1. .770
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note="Organ: heart; Vector: pBluescript; Site 1: 5' of vector Not1; Site 2: 3' of vector EcoRI; Tissue source: dog heart (adult, 30 day - 40 day fetal), right and left atria and ventricle. Dog breed - mixed (beagle, German shepherd, pointer, Irish setter). Library construction: oligo-dT primed"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /tissue_type="heart"
/cell type="heart"
/dev_stage="mixed developmental stages (adult, 30 day -
day Fetal)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /clone_lib="Canine heart normalized cDNA Library
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             72.5%;
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Pred. No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             99;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MD 20850, USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               13;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      linear
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Russell,D., Chen,D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GSS 11-OCT-2002
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REFERENCE
AUTHORS
TITLE
JOURNAL
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CA315228/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FEATURES
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                          Query Match 71.0%;
Best Local Similarity 83.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ORGANISM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: Dr. Jim Lin, University of Iowa
cDNA Library preparation: Dr. M. Bento Soares, University of Iowa
cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              40;
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UI-M-FWO-cbi-b-15-0-UI.rl NIH_BMAP_FWO
IMAGE:6809872 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 GAGGATGAAGCTGAAGAGGAGGAGGAGGAGGAGGAGAGTGTGAAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 sequence: 37-156, > (GGA)n#Simple_repeat (m
82-200, > (GAA)n#Simple_repeat (matched com
> (GGA)n#Simple_repeat (matched compliment)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NIH-MGC http://mgc.nci.nih.gov/.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostc
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
1 (bases 1 to 256)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mus musculus (house mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The following repetitive elements were found in this cDNA sequence: 37-156, >(GGA)n#Simple_repeat (matched compliment) 32-200, >(GAA)n#Simple_repeat (matched compliment) 201-254,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This clone was contributed by the Brain Molecular Anatomy Project
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
  Conservative
                                                                                                                                      /dev stages embryo 13.5,14.5,16.5,17.5dpc"
//lab_hosts = "DH10B (T1 phage resistant)"
//clone_lib="NII_BMAP_FW0"
//notes = "Organ: Brain; Vector: pYX- Asc; Site_1: EcoR I;
//notes = "Organ: Brain; Vector: pYX- Asc; Site_1: EcoR I;
//notes = "Organ: Brain; Vector: pYX- Asc; Site_1: EcoR I;
//notes = "Organ: Brain; Vector: pYX- Asc; Site_1: EcoR I;
//notes = "Organ: Brain; Vector: pXX- Asc; Site_1: EcoR I;
//notes = "Organ: Brain; Vector: pXX- Asc; Site_1: EcoR I;
//notes = "Organ: Brain and Soares, Genome Research, 6:791-806,
//notes = "Organ: Brain and Soares, Genome Research, 6:791-806,
//notes = "Organ: Brain and cDNA was size fraction all agarose
gel. First strand cDNA synthesis was primed with oligo-dT
primer containing a Not I site. Double strand cDNA was
size selected according to mRNA size fraction, ligated
with EcoR I adaptor, digested with NotI and then cloned
directionally into pYX-Asc vector. The library tag
sequence located between the Not I site and the polyA tail
is AGCAGACNG. This library was created for the University
Iowa Brain Anatomy Project (BMAP): 'Gene Discovery in the
Developing Mouse Nervous System', supported by National
Institute of Mental Health (NIMH), Hemin Chin, Ph.D.,
program coordinator."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 tissue_type="whole brain"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              organism="Mus musculus"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            one="IMAGE:6809872"
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87.0%;
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                          Score 36.2; DB 14;
Pred. No. 1.3e+02;
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Pred. No. 1.3e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mismatches
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                                                     Length 256;
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musculus
  Indels
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ACCESSION
VERSION
                                                                                                              RESULT 12
CB625989
LOCUS
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COMMENT
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                                                                                        DEFINITION
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                                                                                                                                                                                                                                                                                                                        Matches
                                                                                                                                                                                                                                                                                                                                                                   Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              source
                                                                                                                                                                                                                                                                                                                                                Local Similarity
                                                                                                                                                                                                                                 72
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                                                    ענטטאט 763 bp mRNA linear EST 08-APR OSIIEa15013.f OSIIEa Oryza sativa (indica cultivar-group) cDNA clone OSIIEa15013 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                      39;
CB625989
CB625989.1 GI:29620978
EST.
                                                                                                                                                                                                                                                                        1 GAGGATGAAGCTGAAGAGGAGGAGGAGGAGGAAGAGTGTGA 44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WashU-HHMI Mouse EST Project
Washington University School of MedicineP
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 (bases 1 to 490)
Marra, M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dub, Geisel, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M., Schellenberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, B., Theising, B., Wylie, T., Lennon, G., Soares, B., Wilson, R. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AMBYSSZI 490 bp mRNA linear EST 06-APR-1991 vyl3s07.rl Stratagene mouse macrophage (#937366) Mus musculus cDNA clone IMAGE:1295340 5' similar to gb:X56135 Mouse mRNA for profibrmosin alaha (Morree).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Unpublished (1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Seq primer: -28m13 rev1 ET from Amersham
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Tel: 314 286 1800
Fax: 314 286 1810
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mus musculus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mus musculus (house mouse)
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                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                  /clone_lib="Stratagene mouse macrophage (#937306)"
/note="Organ: blood; Vector: pBluescript SK-; Site 1:
EcoRI; Site 2: XhoI; Cloned unidirectionally. Primer:
Oligo dT. WEHI-3 cell line. Average insert size: 1.5 kb;
Uni-ZAP XR Vector; ~5' adaptor sequence: 5' GAATTCGGCACGAG
3' ~3' adaptor sequence: 5' CTCGAGTTTTTTTTTTTTTTTT 3'"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /mol type="mRNA"
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/clone="IMAGE:1295340"
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/lab_host="SOLR (kanamycin resistant)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      organism="Mus musculus"
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88.6%;
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Pred. No. 1.5e+02;
                                                                                                                                                                                                                                                                                                                                                                   Length 490
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CB625990/c
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Moryza sativa (indica cultivar-group)

Eukaryota, Viridiplantae, Streptophyta; Embryophyta; T

Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poac

Ehrhartoideae; Oryzeae; Oryza.

E 1 (bases 1 to 822)

S Jantasuriyarat, C., Lu,G., Gowda,M., Hatfield,J., Zhou,

Kudrna,D., Dean,R., Soderlund,C., Wing,R. and Wang,G.,

Large-scale identification of ESTs involved in the int

Detween rice and Magnaporthe grisea

L Unpublished (2003)
Contact: Rod Wing
Arizona Genomics Institute
University of Arizona
Biological Sciences West, 448A, p
85721-0088, USA
Tel: 520 626 3967
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                                                                                                                                                                                                                                                                                                                                       CB625990 mRNA linear EST 0. OSIIEAL5013.r OSIIEA Oryza sativa (indica cultivar-group)
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39; Conserv
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Jantasuriyarat C., Lu.G., Gowda,M., Hatfield,J., Zhou,B., Mazur,E.,
Kudrna,D., Dean,R., Soderlund,C., Wing,R. and Wang,G.

Large-scale identification of ESTs involved in the interaction
Unpublished (2003)

Contact: Rod Wing

Contact: Rod Wing

Contact: Rod Wing
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BACKWARD: gga aac agc tat gac cat g
Plate: 15 row: O column: 13
Seq primer: gta aaa cga cgg cca gtg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Email: http://genome.arizona.edu
PCR PRimers
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Fax: 520 621 9288
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Biological Sciences West, 448A,
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Oryza sativa (indica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Em
Spermatophyta; Magnoliophyta; Liliopsida;
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/note="Vector: pBluescript
xhol; Lesion Mimic SPL 11"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /tissue_type="Leaf"
/dev_stage="3 week"
/lab_host="DH10B"
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/mol_type="mRNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              cultivar="IR36"
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                                                                                                                                                                                                                                                                                                                    GI:29620979
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88.6%;
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Pred. No. 1.6e+02;
0; Mismatches 5
                                 P.O.
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                            Box 210088, Tucson,
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a; Poales; Poaceae;
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a; Poales; Poaceae;
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                                                                                                                                 interaction
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                                                                                                                                                                                                                                                                                                            Contact: David L. Adelson
Animal Breeding and Genetics
Texas A&M University
                                                                                                                                                                                                                                                                  Tel: 9798452616
                                                                                                                                                                                                                                                                                             Animal Science Dept., TAMU-2471,
                                                                                                                                                                                                                                                                                                                                                                      Unpublished (2002)
                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus. 1 (bases 1 to 365) Adelson, D.L. and Gill, C.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sus scrofa (pig)
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Plate: 15 row: 0 column: 13
Seq primer: gga aac agc tat gac cat
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Email: http://genome.arizona.edu
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                            david.adelson@tamu.edu.
Location/Qualifiers
//OJ type="mRNA"

//OD xref="taxon:9823"

/db xref="taxon:9823"

/clone lib="CSEQFXLJ8 pig thyroid and parathyroid"

/note="Organ: thyroid and parathyroid gland; Vector:

pBluescript SK+; Site 1: NotI; Site 2: EcoRI; sequence 5:

of the insert (5'-NNN. ...NNNInsert)

GCGAATTGGAGCTCCACCGCGGTGGCGGCTCGAG. Sequence 3: of

the insert (AAGAATTCGATATCAAGCTTATCGATACCGTCGAG.

the inserts (AAGAATTCGATATCAAGCTTATCGATACCGTCGAG.

non-normalized library, sequenced 3: with M13R primer."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /clone="OSITEA15013"
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XhoI, Lesion Mimic SPL 11"
                                                                                                                                                                            organism="Sus scrofa"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /organism="Oryza sativa (indica cultivar-group)"
/mol_type="mRNA"
/cultivar="IR36"
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88.6%;
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J thyroid and
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Query Match Best Local Similarity

Matches

Conservative

٥,

Score 35.4; DB 12; Pred. No. 2e+02; 0; Mismatches 6;

Length 365;

0

Gaps

0

69.4**%**; 86.7**%**;

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AUTHORS
TITLE
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BQ294503
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Search completed: March 2,
Job time : 2156 secs
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                                                                                                                                                                  Query Match 69.4%; Score 35.4; DB 13; Length 378; Best Local Similarity 86.7%; Pred. No. 2e+02; Matches 39; Conservative 0; Mismatches 6; Indels 0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Periplaneta americana (American cockroach)

SM Periplaneta emericana
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Orthopteroidea; Dictyoptera; Blattaria; Blattoidea;
Blattidae; Periplaneta

1 (bases 1 to 378)

2 1 (bases 1 to 378)

3 Zhou, Z.W., Liu, Z.G. and Gao, B.
The construction of Periplaneta americana nymph cDNA library and
1964 immunology screen
1964 immunology screen
1964 immunology screen
1066, Bayi Street, Nanchang, Jiangxi, P.R.C.
1067, Bayi Street, Nanchang, Jiangxi, P.R.C.
1068 Bayi Street, Nanchang, Jiangxi, P.R.C.
1078 Email: Zhouzhenwen28@hotmail.com.
1788 Location/Qualifiers
1788
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                                                                                  BQ294503 378 bp mRNA linear EST 15-MAY-2002 Periplaneta americana Lambda Express library Periplaneta americana cDNA clone 5, mRNA sequence.
BQ294503 GI:20803437
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/lab_host="E.coli NM522"
/clone_lib="Periplaneta americana Lambda Express library"
/note="Vector: Lambda Excell; These sequences were
screened by cockroach sensitive patients' IgG4 serum "
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/db_xref="taxon:6978"
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